

FIGURE 1

CGGACGCGTGGGTGCGAGGCGGAAGGTGACCGGGACCGAGCATTTCAGATCTGCTCGGTAGA
 CCTGGTGCACCAACCAC**ATG**TTGGCTGCAAGGCTGGTGTGTCTCCGGACACTACCTTCTAGG
 GTTTTCCACCCAGCTTTTACCAAGGCCTCCCTGTTGTGAAGAATTCCATCAGGAAGAATCA
 ATGGCTGTTAACACCTAGCAGGGAATATGCCACCAAAACAAGAATTGGGATCCGGCGTGGGA
 GAACTGGCCAAGAACTCAAAGAGGCAGCATTGGAACCATCGATGGAAAAATATTAAATTT
 GATCAGATGGGAAGATGGTTTGTGCTGGAGGGGCTGCTGTTGGTCTTGGAGCATTGTGCTA
 CTATGGCTTGGGACTGTCTAATGAGATTGGAGCTATTGAAAAGGCTGTAATTTGGCCTCAGT
 ATGTCAAGGATAGAATTCAATTCACCTATATGTACTTAGCAGGGAGTATTGGTTTAAACAGCT
 TTGTCTGCCATAGCAATCAGCAGAACGCCTGTTCTCATGAACTTCATGATGAGAGGCTCTTG
 GGTGACAATTGGTGTGACCTTTGCAGCCATGGTTGGAGCTGGAATGCTGGTACGATCAATAC
 CATATGACCAGAGCCCAGGCCCAAAGCATCTTGCTTGGTTGCTACATTCTGGTGTGATGGGT
 GCAGTGGTGGCTCCTCTGACAATATTAGGGGGTCTCTTCTCATCAGAGCTGCATGGTACAC
 AGCTGGCATTGTGGGAGGCCTCTCCACTGTGGCCATGTGTGCGCCAGTGAAAAGTTTCTGA
 ACATGGGTGCACCCCTGGGAGTGGGCCTGGGTCTCGTCTTTGTGTCCTCATTGGGATCTATG
 TTTCTTCCACCTACCACCGTGGCTGGTGCCACTCTTTACTCAGTGGCAATGTACGGTGGATT
 AGTCTTTTTTCAGCATGTTCTTCTGTATGATACCCAGAAAGTAATCAAGCGTGCAGAAGTAT
 CACCAATGTATGGAGTTCAAATAATGATCCCATTAACTCGATGCTGAGTATCTACATGGAT
 ACATTAATATATTTATGCGAGTTGCAACTATGCTGGCAACTGGAGGCAACAGAAAGAAAT**TG**
AAGTGACTCAGCTTCTGGCTTCTCTGCTACATCAAATATCTTGTTAATGGGGCAGATATGC
 ATTAATAGTTTTGTACAAGCAGCTTTTCGTTGAAGTTAGAAGATAAGAAACATGTCATCATA
 TTTAAATGTTCCGGTAATGTGATGCCTCAGGTCTGCCTTTTTTTCTGGAGAATAAATGCAGT
 AATCCTCTCCCAAATAAGCACACACATTTTCAATTCTCATGTTTGAGTGATTTTAAATGTT
 TTGGTGAATGTGAAACTAAAGTTTGTGTCATGAGAATGTAAGTCTTTTTTCTACTTTAAAA
 TTTAGTAGGTTCACTGAGTAACTAAAATTTAGCAAACCTGTGTTTGCATATTTTTTGGAGT
 GCAGAAATATTGTAATTAATGTCATAAGTGATTTGGAGCTTTGGTAAAGGGACCAGAGAGAAG
 GAGTCACCTGCAGTCTTTTGTTTTTTAAATACTTAGAACTTAGCACTTGTTGTTATTGATTA
 GTGAGGAGCCAGTAAGAAACATCTGGGTATTTGGAACAAGTGGTCATTGTTACATTCAATTT
 GCTGAACCTTAACAAAACCTGTTTCATCCTGAAACAGGCACAGGTGATGCTTCTCCTGCTGTTG
 CTCTCAGTGCTCTCTTTCCAAATATAGATGTGGTCATGTTTGACTTGTACAGAATGTTAATC
 ATACAGAGAATCCTTGATGGAATTATATATGTGTGTTTTACTTTTGAATGTTACAAAAGGAA
 ATAACCTTAAACATATTCTCAAGAGAAAATATTCAAAGCATGAAATATGTTGCTTTTCCAG
 AATACAAACAGTATACTCATG

FIGURE 2

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSREYATKTRIGIRRGRTGQEL
KEAALEPSMEKIFKIDQMGRWFWAGGAAVGLGALCYYGGLSNEIGAIEKAVIWPQYVKDRI
HSTYMYLAGSIGLTALSAIAISRTPLVMNFMMRGSWVTIGVTFAMVGAGMLVRSIPYDQSP
GPKHLAWLLHSGVMGAVVAPLTILGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL
GVGLGLV FVSSLGSMFLPPTTVAGATLYSVAMYGGLVLFSMFLLYDTQKVIKRAEVSPMYGV
QKYDPINSMLSIYMDTLNIFMRVATMLATGGNRKK

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FIGURE 3

GAAGGCTGCCTCGCTGGTCCGAATTTCGGTGGCGCCACGTCGCGCCCGTCTCCGCCCTTCTGCAT
CGCGGCTTCGGCGGCTTCCACCTAGACACCTAACAGTCGCGGAGCGCGCCGCGTGTGAGGG
GGTCGGCAGCGGGAGTCGGGCGGTCTTGTGCATCTTGGCTACCTGTGGGTGCAAGATGTCGG
ACATCGGAGACTGGTTTCAGGAGCATCCCGGCGATCACGCGCTATTGGTTCGCCGCCACCGTC
GCCGTGCCCTTGGTCGGCAACTCGGCTCATCAGCCCGGCTACCTCTTCCCTCTGGCCCGA
AGCCTTCCTTTATCGCTTTCAGATTGGAGGCCAATCACTGCCACCTTTTATTTCCTCTGTGG
GTCCAGGAACCTGGATTCTTTATTGGTCAATTTATATTTCTTATATCAGTATTTCTACGCCA
CTTGAACACAGGAGCTTTTGTATGGGAGGCCAGCAGACTATTTATTCATGCTCCCTCTTAACTG
GATTTGCATCGTGATTACTGGCTTAGCAATGGATATGCAGTTGCTGATGATTCCTCTGTATCA
TGTCACTACTTTATGTCTGGGCCAGCTGAACAGAGACATGATTGTATCATTTTGGTTTGGGA
ACACGATTTAAGGCCCTGCTATTACCCTGGGTATCCTTGGATTCAACTATATCATCGGAGG
CTCGGTAATCAATGAGCTTATTGGAATCTGGTTGGACATCTTATTTTTTCCATAATGTTC
GATACCAATGGACTTGGGAGGAAGAAATTTCTATCCACACCTCAGTTTTTGTACCGCTGG
CTGCCAGTAGGAGAGGAGGAGTATCAGGATTTGGTGTGCCCCCTGCTAGCATGAGCGGAGC
TGCTGATCAGAAATGGCGGAGGCGGAGACACAACCTGGGGCCAGGGCTTTCGACTTGGAGACC
AGTGAAGGGGCGGCCCTCGGGCAGCCGCTCCTCTCAAGCCACATTTCCCTCCAGTGCTGGGTG
CACTTAAACATGCGCTTCTGGCTAACACTGTTGGACCTGACCCACACTGAATGTAGTCTTTC
AGTACGAGACAAAGTTTCTTAAATCCCGAAGAAAAATATAAGTGTCCCAAGTTTTCAGCAT
TCTCATTTCAAGTCTTACTGCTGTGAAGAACAATACCAACTGTGCAAAATGCAAAACTGAC
TACATTTTTTGGTGTCTTCTCTCTCCCTTTCCGTCTGAATAATGGGTTTTAGCGGGTCTT
AATCTGCTGGCATTGAGCTGGGCTGGGTACCAACCTTCCCAAAAGGACCTTATCTCTT
TCTTGACACATGCTCTCTCCACTTTTCCCAACCCCACTTTGCAACTAGAAAAAGTTG
CCCATAAAATGCTCTGCCCTTGACAGGTTCTGTTATTTATTGACTTTTGCCAAGCTGGTC
ACAACAATCATATTCAGCTTATTTTCCCTTTTGGTGGCAGAACTGTTACCAATAGGGGGAG
AAGACGACCACGGATGAAGCGTTTCTCAGCTTTTGGAAATGCTTCGACTGACATCCGTTGTT
AACCCTTGGCACTCTTCAGATATTTTTTATAAAAAAAGTACCCTGAGTTCATGAGGGCCA
CAGATTGGTTATTAATGAGATACGAGGGTTGGTGTGGGTGTTTGTTCCTGAGCTAAGTGA
TCAAGACTGTAGTGGAGTTGCAGCTAACATGGGTAGGTTAAACCATGGGGGATGCACCCC
TTTGCGCTTTCATATGTAGCCCTACTGGCTTTGTGTAGCTGGAGTAGTTGGGTGCTTTGTGT
TAGGAGGATCCAGATCATGTTGGCTACAGGAGATGCTCTCTTTGAGAGGTCCTGGGCATTG
ATTCCCATTTCAATTCATCTCGGATATGTGTTCAATTGAGTAAGGAGGAGAGACCTCATA
CGCTATTTAAATGTCATTTTGTGCTATCCCCGTTTGTGTCATGTTTCAATTAATTGT
GAGGAAGCGCGAGCTCCTCTCTGCACGTAGATCATTTTTTAAAGCTAATGTAAGCACATCTA
AGGGAATAACATGATTTAAGGTTGAAATGGCTTAGAATCATTGGGTTTGGGGTGTGTTA
TTTTGAGTCAATGAATGTACAAGCTCTGTGAATCAGACCAGCTTAAATACCCACACCTTTTT
TCGTAGTGTGGGCTTTTCTATCAGAGCTTGGCTCATAACCAAATAAAGTTTTTTGAAGGCCA
TGGCTTTGCACAGTTATTTTTATTTATGACGTATATCTGAAAGCAGACTGTTAGGAGCAGT
ATTGAGTGGCTGTACACTTTGAGGCAACTAAAAGGCTTCAAACGTTTGTATCAGTTTCTT
TTCAGGAACATCTGTGCTCTAACAGTATGACTATTCTTTCCCTTCTTGAATAGAGTTTGTGTG
GTGTGTTATCCTAGGAAATGAGAGTTGGCAACAACACTTTCGACTTTGAATAGAGTTTGTGTG
TACTTCTCCATATTTAATTTATATGATAAAATAGTGGGAGAGTCTGAACCTTAACTGTCA
TGTTTTGTTGTTTCATCTGTGGCCACAATAAAGTTTACTGTGAAATTTAGAGGCCATTACT
CCAATATTTGTGACGTACACTCATTTGACAGGCGTGGAGACTCATTTGTATGTATAAGAAAT
TTTCTGACAGTGAAGTGACCCGGAGTCTCTGGTGTACCTCTACCAGTCAGCTGCCGCGAG
CAGTCATTTTTTCTAAAGGTTTACAAGTATTTAGAATTTTCAGTTTCAGGGCAAAATGTTT
ATGAAGTTATCTCTTAAACATGGTTAGGAAGCTGATGACGTTTGTGATTTGTCTGGATT
ATGTTTCTGGAATTAATTTTACCAAAACAAGCTATTGTGATTTTGAATGACAAGGCAAAACA
TGACAGTGGATTCTCTTTACAAATGGAATAAAATCCTTATTTGTATGAAGGACTTCCC
TTTTTGTAACATAATCTTTTATTTGGTAAAAATGTAAATTAATGTGCAACTTG

FIGURE 4

MSDIGDWFRSIPAITRYWFAATVAVPLVVGKLGGLISPAYLFLWPEAFLYRFQIWRPITATFYF
PVGPGTGFLYLVLNLYFLYQYSTRLETGAFDGRPADYLEMLLFNWICIVITGLAMDMLMIP
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIIGGSVINELIGNLVGHLYFFL
MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRAADQNGGGGRHNWQGQFRL
GDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

MSDIGDWFRSIPAITRYWFAATVAVPLVVGKLGGLISPAYLFLWPEAFLYRFQIWRPITATFYF
PVGPGTGFLYLVLNLYFLYQYSTRLETGAFDGRPADYLEMLLFNWICIVITGLAMDMLMIP
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIIGGSVINELIGNLVGHLYFFL
MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRAADQNGGGGRHNWQGQFRL
GDQ

FIGURE 5

GGGGCCGCGGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTTGCATTAAGTGGTTG
 GTAGCTTCTATCCTGGGGGCTGAGCGACTGCGGGCCAGCTCTTCCCCTACTCCCTCTCGGCT
 CCTTGTGGCCCAAAGGCCTAACCGGGGTCCGGCGGTCTGGCCTAGGGATCTTCCCGTTGCC
 CCTTTGGGGCGGGATGGCTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGGAGAGCATCG
 CGGGGTTCCTGCGAGGCCAGACTGGTCCATCCCCATCTTGGACTTTGTGGAACAGAAATGT
 GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCCAGAGCCGGTGATTTTGGT
 GGCCTGTGTTCCCTTGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATTC
 ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGTTACCTCAAAGAAATTGGAATT
 AATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAGGC
 CATTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCCAGA
 AAAACATTGAAATGCAGCTGCAAGCCATTTCGAATAATTCAAGAGAGAAATGGTGTATTACCT
 GACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAATCCT
 GAGGGAAGTTCTTAGAAAATCAAAGAGGAATATGACCAGGAAGAAGAAAGGAAGAGGAAAA
 AACAGTTATCAGAGGCTAAAACAGAAGAGCCACAGTGCATTCCAGTGAAGCTGCAATAATG
 AATAATTCCAAGGGGATGGTGAACATTTTGCACACCCACCTCAGAAGTTAAATGCATTT
 TGCTAATCAGTCAATAGAACCTTTGGGAAGAAAAGTGAAAGGTCTGAAACTTCCTCCCTCC
 CACAAAAAGGCCTGAAGATTCTGGCTTAGAGCATGCGAGCATTGAAGGACCAATAGCAAAC
 TTATCAGTACTTGGAACAGAAGAACTTCGGCAACGAGAACACTATCTCAAGCAGAAGAGAGA
 TAAGTTGATGTCCATGAGAAAGGATATGAGGACTAAACAGATACAAAATATGGAGCAGAAAG
 GAAAACCCACTGGGGAGGTAGAGGAAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAAG
 CAAACATTACTAAAGAGGAGATTGCTTGACAGAGAACTCAAAGAAGAAGTTATTAATAAGTA
 ATAATTAAGAACAATTTAACAAAATGGAAGTTCAAATTGTCTTAAAAATAAATTATTTAGTC
 CTTACACTG

FIGURE 6

MAAEEEEDEVEWVVESIAGFLRGPDWSIPILDFVEQKCEVNCKGGHVITPGSPEPVILVACVP
LVFDDEEESKLTYTEIHQEYKELVEKLLEGYLKEIGINEDQFQEACTSPLAKTHTSQAILQP
VLAEDFTIFKAMMVQKNIEMLQAIRIIQERNGVLPDCLTDGSDVVSDLEHEEMKILREVL
RKSKEEYDQEEERKRKKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPPSEVKMHFANQS
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPIANLSVLGTEELRQREHYLKQKRDKLMS
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEKQTLKRRLLAEKLEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

FIGURE 7

GGGCACAGCACATGTGAAGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT
TCATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAA
TTAATGAAGATCAATTTCAAGAAGCATGCACCTTCTCCTCTTGCAAAGACCCATACATCACAG
GCCATTTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC
AGAAAAACATTGAAATGCAGCTGCAAGCCATTCTGAATAATCAAGAGAGAAATGGTGTATTA
CCTGACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAAAT
CCTGAGGGAAGTTCTTAGAAAAATCAAAGAGGAATATGACCAGGAA

FIGURE 8

GCGTGGTTTTGTTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTG
 TAGCTTCTCCACGTATGGACCCATAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTG
 TCTCAGCTCTAGGATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTAACAAAC
 AGTGAATGCAAAACAGTCTGTAGTCATCCTGTAATATGCTCCTGTCAACAATGTATAC
 ATTCTCTAGGTGCCATATTCATGTCTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATT
 CTGCCAATGAAGAAACAAGTATGATTATCTTCCAACCTACTGTGAATGTGTGCTCAGAACTG
 GTGAAGCTAGTTTTCTGTGTGCTTGTGTCATTCGTGTTATAAAGAAAGATCATCAAAGTAG
 AAATTTGAAATATGCTTCTCGGAAGGAATTCCTGATTTTCATGAAGTGGTCCATTCCTGCCT
 TTCTTTATTTCTGGATAACTTGATTGTCTTCTATGTCTGTCTATCTTCAACCAGCCATG
 GCTGTTATCTTCTCAAATTTTAGCATTATAACAACAGCTCTTCTATTACAGGATAGTGTGAA
 GAGGCGCTAAACTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCCT
 TGACTGCCGGGACTAAAACTTTACAGCACAACTTGGCAGGACGTGGATTTTCATCAGATGCC
 TTTTTCAGCCCTTCCAATTCCTGCCTTCTTTTTCAGAAGTGAGGTGCCAGAAAGACAAATTG
 TACAGCAAGGGAATGGACTTTTCTGAAGCTAAATGGAACAGGCAGAGATTTTCAGTC
 ACATCCGTCTTGGCATGGGCCATGTTCTTATTATAGTCCAGTGTTTTATTTCTTCAATGGCT
 AATATCTATAATGAAAAGATACTGAAGGAGGGGAACAGCTCACTGAAAGCATCTTCATACA
 GAACAGCAAACTCTATTTCTTGGCATTCTGTTTAATGGGCTGACTCTGGGCCCTTCAGAGGA
 GTAACCGTGATCAGATTAAGAAGCTGTGGATTTTTTATGGCCACAGTGCAATTTTCAGTAGCC
 CTTATTTTTTGAACGTGCATTCCAGGGCCTTTCAGTGGCTTTCATCTGAGATTCTGGATAA
 CATGTTCCATGTCTTGATGGCCAGGTTACCACGTGCTATTATCACAAAGTGTCTGTCTGTG
 TCTTTGACTTCAGGCCCTCCCTGGAATTTTTCTTGGAGCCCCATCAGTCTTCTCTCTATA
 TTTATTTATATGCCAGCAAGCCTCAAGTTCGGGAATACGCACCTAGGCAAGAAAGGATCCG
 AGATCTAAGTGGCAATCTTTGGGAGCGTTCCAGTGGGGATGGAGAAGACATGAAGACTTA
 CCAAACCCAAGATGATGAGTCAGATGAAGATACTTTCTAACTGGTACCCACATAGTTTGGCA
 GCTCTCTTGAACCTTATTTTCACATTTTCAGTGTTTGTAAATATTTATCTTTTCACTTTGATA
 AACCAGAAATGTTTCTAAATCCTAATATCTTTGCATATATCTAGCTACTCCCATAATGGTT
 CCATCCAAGGCTTAGAGTACCCAAAGGCTAAGAAATTCATAAGAACTGATACAGGAGTAACA
 ATATGAAGAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTTATATGTGCAGATTAT
 TTTCTTGGCCTTCAAGCTTCCAAAAAAGCTTGTAAATCATGTTAGCTATAGCTTGTATAT
 ACACATAGAGATCAATTTGGCCAAATATTCACAATCATGTAGTTTACATGCCCCAAAGT
 CTTCCTTTTTTAACATTATAAAAGCTAGGTTGTCTCTTGAATTTTGGAGCCCTAGAGATAGT
 CATTTTGCAGTAAGAGCAACGGGACCCTTCTAAAAACGTTGGTTGAAGGACCTAAATAC
 CTGGCCATACCATAGATTTGGGATGATGTAGTCTGTGCTAAATATTTTGTCTGAAGAAGCAGT
 TTCTCAGACACAACTCTCAGAAATTTAATTTTTAGAAATTCATGGGAAATGGATTTTTGT
 AATAATCTTTTGATGTTTTAAACATTTGGTTCCCTAGTCCACATAGTTACCACCTGTATTTTA
 AGTCATTTAAACAAGCCACGGTGGGGCTTTTTTCTCCTCAGTTTGAGGAGAAAAATCTTGAT
 GTCATTACTCCTGAATTATACATTTTGGAGAATAAGAGGGCATTTTATTTTATTTAGTTACT
 AATTCAAGCTGTGACTATTGTATATCTTCCAAGAGTTGAAATGCTGGCTTCAGAATCATAC
 CAGATTGTGAGTGAAGCTGATGCCTAGGAACCTTTTAAAGGGATCCTTTCAAAGGATCACTT
 AGCAAAACATGTTGACTTTTAACTGATGTATGAATATTAATCATCTAAAAATAGAAAGACC
 AGTAATATATAAGTCACTTTACAGTGCTACTTCACACTTAAAGTGCAATGGTATTTTTTCATG
 GATTTTGTGATGCAGCCAGTTAAGCTCTCGTAGATAGAGAAGTCAAGGTGATAGATGATATTA
 AAATTAGCAACAAGAGTGACTTGGCTCAGGGTCATGCAGCTGGTGATGATAGAAAGAGTGGG
 CTTTAACTGGCAGGCCTGTATGTTTACAGACTACCATACTGTAATATGAGCTTTATGGTGT
 CATTTCTCAGAACTTATACATTTCTGCTCTCCTTCTCCTAAGTTTCATGCAGATGAATATA
 AGGTAATATACATTATATAATTCATTTGTGATATCCACAATAATATGACTGGCAAGAATTG
 GTGGAATTTGTAATTAATAATTTATTAACCT

FIGURE 9

MEKQCCSHPVICSLSTMYTFLLGAIFFIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK
LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLPAMAV
IFS NFSIITTALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFF
SPSNSCLLFRSECPRKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISSMANI
YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFYGHSAFSVALI
FVTAQQGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFI
YNASKPQVPEYAPRQERIRDLSGNLWERSSSGDGEELERLTKPKSDEDEDTF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

FIGURE 10

CGTGCCTGCGCAATGGGTGTCGGGTCCGCTTTTTCCCAATCCGGACGTAATCGTGGTTTTTG
TTCTGCAATAGGCGGCTTAGAGGGAGGGCTTTTTTCGCCATACCTACTGTAGCTTCTCCAC
GTATGGACCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTA AAAACAGTGAATGGAA
AAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCACCAATGTATACATTCCCTGCTAGG
TGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG
AAAACAAGTATGATTATCTTCCAAC TACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT
TTCTGTGTGCTTGTGTCA TTCTGTGTATATAAGAAAAGATCATCAAAGTAGAAATTTGAAATA
TGCTTCCTGGAAGGAATTCTCTGATTCATGAAGTGGTCCATTCCCTGCCTTTCTTTATTTCC
TGGATAACTTGATTGCTTCTATGTCTGTCTTCAACCAGCCATGGCTGTTATCTTC
TCAAATTTTAGCATTATAACAACAGCTCTTCTATTTCAGGATAGTGTGAAGAGGCGCTAAA
CTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCCTTGACTGCCGGGA
CTAAAAC TTA

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGGCCGGCTTGGCTAGCGCGCGGCGGCC
GTGGCTAAGGCTGCTACGAAGCAGAGCTTGGGAGGAGCGAGCGGCTCGGGGCGAGGAGCAT
CCCCCTACCAGGTCCCAAGCGCGCTGCCCCGCGGGTTCATGGCCAAAGGAGAGCGCCGAG
ACGGCGTCCCGCGGGGGGCTGCTACCCACCAGCATCCTCCAAGCACTGAACGCCCGGCCCA
GGTGAAGAAAGAACCGAAAAAGAAACAACTGGTGTGTTTGCACAAAGCTTGTCTATG
CACTTGGGGGAGCGCCCTACAGGTGACGGGCTGTGCCCTGGGTTTCTCTTCAGATCTAC
CTATTGGC**ATG**TGGCTCAGGTGGGCGCTTCTCTGCTCCATCATCCTGTTTGTGGGCGGAGC
CTGGGATGCCATCAGACGCCCTGGTGGGCGCTGTCATCAGAAATCCCCCTGGACCTGCC
TGGTTCGCCTTATGCCCTGGATCATCTTCCAGCGCCCTGGCCGTCATTGCCATCTCTCT
ATCTGCTTCGTGCCGACTTCCACAGCGCGAGACCTATTGGTACCTGCTTTTCTATTGCCT
CTTTGAAACAATGGTCACGTGTTTCCATGTTCCCTACTCGGCTCTACCATGTGTCATCAGCA
ACCGAGCAGACTGAGCGGGATTCTGCCACCGCCCTCATCGGATGACTGTGGAAGTCGGGCAG
AGTGCTGGGACGGCGCATCAGGGCAAAATCGTGGGCCAAGCAGACAGCGCTTGTTCAGG
ACTTCAATAGCTCTACAGTAGCTTCAAAAGTGCCAACCATACATAGGCACCACCTCACAC
AGGGAACCGAAAGGATACCTGCTGGCAGCGGGGTCATTGTCTGTATATATAATCTG
TGCTGTACCTCTGACTCTGGGCGTGGCGGAGCAGAGAGAACCCTATGAAGCCAGCAGCTG
AGCCAATCGCCTACTTCCGGGGCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCT
ATTACTGGCTTCTCTTCACTCTCTGGCTTTCATGCTGGTGGGAGGGAACCTTGTCTGT
TGCACCTACACTTGGGCTTCCGAATGAATTCAGAATCTACTCTCGGCCATCATGTGCTCT
CGGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGCAGCT
GTATATGTTGGGATCTCATCAGCAGTGGCAATTTCTCATCTTGGTGGCCCTCATGGAGAGTAA
CCTCATCTTACATATCGGTAGCTGTGCGAGCTGGCATAGTGTGGCAGCTGCCCTTCTTAC
TACCCTGGTCCATGCTGCCGTGATGTCATTGACGACTTCCATCTGAAGCAGCCCCCATCTCAT
GGAACCGAGCCCATCTTCTTCTCTCTCTATGCTTCTTCAACCAAGTTTGCCTCTGGAGTGTC
ACTGGGCATTCTTACCCTAGCTTGGACTTTCGAGGATACAGACCGGTGGCTGCTGCGAGC
CGGAAGCTGTCAAGTTTAACTGAACATGCTCGTGACCATGGCTCCCATAGTTCTCATCTCTG
CTGGGCGCTGCTGCTCTTCAAATAGTACCACCTTATGATGAGGAGAGCGGGCGGCAAGAA
GGCCCTGACGCACTGAGGACGAGGCCAGCAGCTTGTGGCTGCTCAGAAACAGACTCCACAG
AGCTGGCTAGCATCCTCT**TAG**GGGCCGCCACGTTGCCGAAGCCACCATGCAGAAGGCCAGG
AAGGGATCAGGACTGTCTGCCCCGTGCTGACAGCTGGACTGCAGGTGCTAGGAAGGAA
CTGAAGACTCAAGGAGGTGGCCAGGACACTGTGCTGCTCACTGTGGGCGCGGCTGCTCTG
TGCGCTCTGCTTCTCTCTGCTTCTGCTGCTGTGGGGCCAAGCCCTGGGCTGCCACTGTGAATA
TGCCAAGGACTGATCGGGCTAGCCCGGAACTAATGTAGAACCTTTTTTTTACAGAGCC
TAATTAATAACTTAATGACTGTGTACATAGCAATGTGTGTGTATGTATGTCTGTGAGCTA
TTAATGTATTAAATTTTCTATAAAAGCTGGAAGC

FIGURE 12

MWLRWALSLPPSSCLWAEPPGMPSQTPWWASASANPPGPAWVALCPGSSSPRPWPSLPTSSSG
SCPTSHRTARPIGTCTFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVL
GTAIQGQIVGQADTPCFQDFNSSTVASQSANHTHGTSHRETQKAYLLAAGVIVCIYIICAV
ILILGVREQREFYEAQQSEPIAYFRGLRLVMSHGPHYIKLITGFLFTSLAFMLVEGNFVLFCT
YTLGFRNEFQNLALLAIMLSATLTIPWQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLI
ITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVFFTKFASGVSLG
ISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLFKMYPIDEERRRQNKAL
QALRDEASSSGCSETDSTELASIL

12/330
SCPTSHRTARPIGTCTFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVL
GTAIQGQIVGQADTPCFQDFNSSTVASQSANHTHGTSHRETQKAYLLAAGVIVCIYIICAV
ILILGVREQREFYEAQQSEPIAYFRGLRLVMSHGPHYIKLITGFLFTSLAFMLVEGNFVLFCT
YTLGFRNEFQNLALLAIMLSATLTIPWQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLI
ITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVFFTKFASGVSLG
ISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLFKMYPIDEERRRQNKAL
QALRDEASSSGCSETDSTELASIL

GGGAAACGCAAAAGGCATACCTGCTGGCAGCGGGGTCATTGTCTGTATCTATATAATCTGT
GCTGTCATCCTGATCCTGGGCGTGC GGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTGA
GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCTTA
TTACTGGCTTCCTCTTACCTCCTTGGCTTTCATGCTGGTGGAGGGGAACCTTTGTCTTGTTT
TGCACCTACACCTTGGGCTTCCGCAATGAATTCCAGAATCTACTCCTGGCCATCATGCTCTC
GGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCTG
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC
CTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT
ACCTTGGTCCATGCTGCCTGATGTCA TTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG
GAACCAGGCCAT

FIGURE 14

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTACAAAAGGTGCAGGT
ATGAGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAAACAGAAAACCTGTTAGAAATGT
GGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCT
TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT
CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG
CAGTTTATGCATTGCTACCATTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAA
GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGCTACTTGGAAATACTGAGTTGTTTAGG
ACTTTCATTGTGGCAAACCTCCAGAAAACAACCTTTTTGCTGCACATGTAAGTGGAGCTG
TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTCAGACCATCCTTTCCTACCAAATG
CAGCCCAAAATCCATGGCAAACAAGTCTTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG
AGTAAGTGCACCTTAGCATGCTGACTTGTCTCATCAGTTTGCACAGTGGCAATTTTGGGACTG
ATTTAGAACAGAACTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACT
ACTGCAGCAGAATGGTCTATGTCATTTTCCTTCTTTGGTTTTTTCCTGACTTACATTCGTGA
TTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTACATGGATTAACCTCTATGACACTG
CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCAGAGATATTTCATGAAAGGAT
AAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGGTTACAGAAGTTGCTTA
TTCTTCTCTGAAATTTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA
ATCAGGAAACATGAAAGAAGCCATTTGATAGATTATCTAAAGGATATCATCAAGAAGACTA
TTAAAAACACCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAGACTATG

FIGURE 15

MWWFQQGLSFLPSALVIWTSAAFI FSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI
AAVLCIATIIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSG
AVLTFGMGSLYMFVQTILSYQM QPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFG
TDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFQKISLRVEANLHGLTLYD
TAPCPINNERTRLLSRDI

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FIGURE 16

CGGACGCTTGGGCNCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT
TCCGTCTCTCGGGTCTTTTCCTGGTCCCAGGCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
GTGCTTCGCGCTTCCGGAGAAAATCAGCGGTCTAATTAATTCCTCTGGTTTGTGAAGCAGT
TACCAAGAATCTTCAACCCTTTCCACAAAAGCTAATTGAGTACACGTTCTGTTGAGTACA
CGTTCCCTGTTGATTTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTGTGAA
GTTGTAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCT
TCAGCCCTTGTAAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACT
CCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC

FIGURE 17

CCCACGCGTCCGCCCCGCGCTGCGTCCCGGAGTGCAAGTGAGCTTCTCGGCTGCCCGCGGG
 CCGGGGTGCGGAGCCGACATGCGCCCGCTTCTCGGCCTCCTTCTGGTCTTCGCCGGCTGCAC
 CTTGCGCTTGTACTTGCTGTGCGACGCGACTGCCCGCGGGCGGAGACTGGGCTCCACCGAGG
 AGGCTGGAGGCAGGTCGCTGTGGTTCCCTCCGACCTGGCAGAGCTGCCGGAGCTCTCTGAG
 GTCCTTCGAGAGTACCGGAAGGAGCACCAGGCCTACGTGTTCTGCTCTTCTGCGGCGCCTA
 CCTCTACAAACAGGGCTTTGCCATCCCCGGCTCCAGCTTCCTGAATGTTTTAGCTGGTGCCT
 TGTTTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTTGACCTCGGTGGGTGCCACATGC
 TGCTACCTGCTCTCCAGTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCTGATAAAAGT
 GGCCCTGCTGCAGAGAAAGGTGGAGGAGAACAGAAACAGCTTGTTTTTTTTCTTATTGTTTT
 TGAGACTTTTCCCCATGACACCAAACCTGGTTCTTGAACCTCTCGGCCCAATTCTGAACATT
 CCCATCGTGAGTTCTTCTTCTCAGTTCTTATCGGTTTGATCCCATATAATTTTCATCTGTGT
 GCAGACAGGGTCCATCCTGTCAACCCTAACCTCTCTGGATGCTCTTTTCTCCTGGGACACTG
 TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAAATCCTGGAACCCTATTAAAAAATTT
 AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACACAGTAGAAAAGA
 CACATGACTCTGGATTTTCTGTTTGCCACATCCCTGGACTCAGTTGCTTATTTGTGTAATGGA
 TGTGGTCTCTAAAGCCCCCATTGTTTTTGATTGCCTTCTATAGGTGATGTGGACACTGTG
 CATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGTATTACATCAGGT
 TTTCAAACCGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCCTAGAAAATGCTGTTTGT
 GGCCGGGCGCGGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCCGGTGATTC
 ACAAGGTGAGGAGTTCAAGACCAGCCTGGCCAAGATGGTGAAATCCTGTCTCTAATAAAAAAT
 ACAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGTAATCCAGCTACTCGGGAGGCTGAGGC
 AGGAGAATTGCTTGAACCAAGGTGGCAGAGGTTGCAGTAAGCCAAGATCACACCCTGCACCT
 CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

FIGURE 18

MRPLLGLLLVFAGCTFALYLLSTRLPRGRRLGSTEEAGGRSLWFPSDLAELRESEVLREYR
KEHQAYVFLLEFCGAYLYKQGFAIPGSSFLNVLAGALFGPWLGLLLCCVLTSVGATCCYLLSS
IFGKQLVVSYPDPKVALLQRKVEENRNSLFFFLLFLRLFPMTPNWFLNLSAPILNIPIVQFF
FSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKLLAIAMVALIPGTLIKKFSQKHLQ
LNETSTANHIHSRKDT

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

FIGURE 19

CCGAGGCGGGAGGAGCCCGAGGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTT
CCAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAAGTCCAGCTCAGAA
TAGGAAAATAACTTGGGATTTTATATTGGAAGACCATGGATCTTGCTGCCAACGAGATCAGCA
TTTATGACAACTTTTCAGAGACTGTTGATTTGGTGAGACAGACCGCCATCAGTGTGGCATG
TCAGAGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAGAATGAACCTCAGAGACC
CCCCCGCAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT
TGCTCACTGCCTACTTTGTGATTCAACCTTTCAGCCCATTAGCACCTGAGCCAGTGTCTTCT
GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCTTGCCCATTGCCAA
GAAGTACATGTCAGAAAATAAGGGAGTTCCTCTGCATGGGGGTGATGAAGACAGACCCTTTC
CAGACTTTGACCCTGTTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCTGCC
AACTGCACTGGCTGTGCCGAGAAACACCTGAAGGTGATGTCTTGGAAGACGCCCCAAGGAA
ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGGAAAGCCCTGTTGGAGGAAGAGATTC
AGCATTTTTTGTGCCAGTACCCTGAGGCGACAGAAAGGCTTCTCTGAAGGGTTTTTCGCCAAG
TGGTGGCGCTGCTTTCCTGAGCGGTGGTCCCATTCTCTTATCCATGGAGGAGACCTCTGAA
CAGATCACAAATGTTACGTGAGCTTTTTCTGTTTTCACTCACCTGCCATTTCAAAAGATG
CCTCTTTAAACAAGTGCTCCTTTCTTCACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAG
ATGCCTGACCTATTTATCATTTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA
GTGCCGAAGACATTGTGAGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCTG
ACACCACCCACTGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGAT
GGAACCGCTTTCTCAGAAGTGTTAGGAAATAGAAGTGTGCACAGGAACAGCTTCCAGAGCCGA
AAACCAGGTTGAAAGGGGAAAAATAAAAACAAAACGATGAACTGCAAAAA

FIGURE 21

CCACGGTGTC CGTTCTTCGCCCGGCCGCGCAGCTGTCCCCGAGGCGGGAGGAGCCCGAGGGGCG
CGAGCCCCGCATGAATCATTGTAGTCAATCATTTTCCAGTTCTCAGCCGTTCAAGTTGTGATC
AAGGGACACGTGGTTTCCGAACTGCCAGCTCAGAATAGGAAAATAACTTGGGATTTTATATT
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTTATGACAACTTTCAAGAGACTGTTG
ATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCAGAGAAGGCAATTGAAAAATTTATC
AGACAGCTGCTGGAAAAGAATGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT
TGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCACTGCCTACTTTGTGATTCAAC
CTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

1000
900
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700
600
500
400
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200
100
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A
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C
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1000
900
800
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CCACGCGTCCGCCACCGGTCCGGCTGAACACCTCTTCTTTGGAGTCAGCCACTGATGAGC
CAGGTCCCCACTTGCAGCTGCAGCAGCTGCAGCAGCTGCAGAGCGCTGCTCTGGCTGGTG
CCACTGGTGGCCACGTGCTAGACCGTGCCATTGAGCCGCTGGGGCTGCAGTGGGACTGCC
CTCCCCTGCCACCACCAATTGGCAGCCCACTTTCTTGAAGACTTCCAGGCTTTTTGTGCCA
CCCCGAATTGGCGCCCACTTCATGCAGAACAGCTACAGCAACCAATGTCACGTTCCGAAT
GACACGTATGCTAAAGAGCCACGACCTTATGTCAGGTTTCAGGCTCGTGGCGGCTTCCAGGAG
TATGAGCACTGGGACAGCGCGCCAGTGGGAGCGGCTTCCAGGCTGCTATGACATGCT
TGGTGTCTGGAACCTGCGCAGGCGGGCGCGCTGGAGGGGTACGCTACACGGCAGTGTCT
AAGCAGCAGGCAACGACGACCTCATGCCCCTGCTGCACTGGGGGGCGTGTGGCGCCAGT
CGCCAGCCCATTTGGGGCTTGGCGCTGAGGACACTCCCATCCCCGTTGGAACTGTCCZ
CGCGCGGAGACATTTACGAGTACGCTGTAAGCTGGTGCCCAACCATCTCTCGACCTCACT
CTGGAAGCCAGCGCTCTCGGAGACAATCTGGGTGAGTTTCCCTGACACCCACGAGGAGG
CTCACTGCCTCTGGCAGTGACCAAGAGGCCAAAGTAGGACACCCACCGAGTTGTCTCAGG
AGGACCAAGCTCGGCGAGGACGAGTGGTGTGAGCTGTGACAGTGTGAGGCTATGTGGCGT
GGTCCACAGGGCTCTGGAGAGTCCACCAAGCATGATGATTTCCGGCGCCACTGGCCCGAGT
CGGTGAAACCGAGGAGGATCGCGATGATTTCCGGCGCCACTGGCCCGAGTGGCTGAGG
GTCCACTGCGCGCTTTCAACCTGCGCGCTTGACCACTTGAGCTTCTTTATGCTCAGG
CAACTACTCTCTCAACTTCCATGCAAGGTGGGACGACCCAGTCTCATCTCTAGCCAGA
CTCCGAGACCCAGCTGCCCCTATCCCAAGCCCATACCCAGGTACGGAACCAAGTGTACTCG
TGCTCTGCGCTACGGCCCGCTCTCAAGGCTACCTAAGCAGCGCTTCCCCCGAGGAGAT
GCTGCTGCTCAGGCTTTACCAAGAAATGGGTACAGCTGAGATATCAACTTTCGATGACT
TGATGCAACTCAACCACTTGGCGGGCGAATCAACTGACTGTCTCACTACCTGTGTGTC
CCCTGGGTCTGCGAGACTACGTGTGCCCAACCTTGGACTCAGCAACCCAGCGCTTCCG
GTGACCTTTTAAGCCCATCGGTGTGGTGAACCCCAAGCATGCCAGCTGTGAGGAGAAGT
ATGAAGAGTTTGGAGACCCAGGAGACATGCAAGTTCCACTATGGCACCCTACTCTC
AATGCGCAGGCGGTGATGCACTACCTCATCCGCTGGAGCCCTTCACTCCCTGCACTCCA
GCTGCAAAAGGGCGCTTTGACTGCTCCGACCGGAGTTCCACTCGGTGGCGGCGAGCTGGC
AGGCACGCTTGGAGAGCCCTGCCGATGTGAAGGAGCTCATCCCGGAATTTCTTCACTTCTT
GACTTCTGGAGAACAAGCGTTTGAACCTGGGTGCTCTCCAGTGTACCAACGAGAAGGT
AGGCGATGTGGTGTACCCCGCTGGGCGAGCTCTCTCAGGACTTCATCCAGCAGCAGCCG
AGCTCTCGAGTCGGAGTATGTGTGTGACAACTACAGAGTGATGCACTCATCTTTGGC
TACAAGCAGCGGGGCGCGCGGAGGAGGCCCTCAATGTCTTCTATTACTCAAGCTATGA
GGGGGCTGTAGCACTGGACATGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGCATTA
TCAGCAACTTTGGGCGAGACTCCCTGTGAGCTGCTGAAGGAGCCACATCCAATCGCTCTCA
GCTGAGGAGAGCAGCCATCGCTTGTGACGCGCTGACACTAATCACTAGCATCTTCCAGA
CTTGGACGAATCAAGGCATTTCTCGCAGAGGTGACTGTGAGTGGCAGTGTGGCTGTGGCA
CCCCAGCTGGTTGCCATGTAGCCCAACATTAAGCACTCTGACTGCTCAGCTCAGCAAGCCCC
ACCATGGGACGCCAAGACGACGAGCACTGTGAGTGGCCCTGGGTGGCCAGGCACTGTGT
GAGTGGACAAGCACTGGCAGTGGCCCGGATGGAAGACTGCTATTACGCGGTGGCACTTGG
ATGGCAGCTCGGGTGTGACTGCACTAACCCCGTGGCGAAGCTGTGAGCCAGTGCAGTGGC
CTTGATGTAGTAACCTGCTTCACTGACAGCACTGTGGCATCTACTCATCTCAGGCTCCG
GGACACCAGCTGACTGTGTGGCGCTTCTGCATAGGTTGGTGTGTGAGTGGCTGACAGT
CAAGGCTGTGCAAGTCTGTATGGGATGGGCTGCAGTGAAGTGTGTGGCCATCAGACT
GAACTTGACATGGCTGTGTGTGATCTGAGGTGGAATGTGATACACAGCTGATACGCC
GGCAGAGTTTGTAGCGGCACTACGCCCTCTGGGTGCCACATTCCTTGGCACTTTTTCACC
TGGCATTTGGGTTCCGAAAGCCAGATTTGTGTACAGAGCTCAGCGTGGGAACGTCTTGGGCC
CAGGTCACTTACTCTTGTCACTGTATTTCACTCAATGGGAAGTTGGCGGCTTCACTGCCCT
GGCAGACAGCCTACAGCCCTGACCGTGACAGGAGCACTTTGTGTGTGGCAGCCGCCACT
GGCCCTGCACATCTTCCAATTAAGCACTGCTCCCGGCGCGCTCCTTGCCATGAAG
GTGGCCATCCGACAGCTGGCCCTGACCAAGGACGCGACGCAAGCTGTGGTGGGCTGGAGGA
TGCGAAGCTCATGTGTGGTGGCGGGGACCCCTTGAGTGGCGAGCAGGCACTTGGCG
GGAAGCTGTGGCGGCTCTCGCGGCGCATCTCCAGGTGTCTCGGAGAGACGGAATACAAC
CCTCTAGGCGCGCGTGAACACTGGCCAGTCCGGCTCTGGCGCCCGCTGGGACGCCAGGGGTGA
CGCCGGAGGCCCTCCGACAGAGTCCGCGGGAACACCCCGGGTGGGACGCCAGGGGTGA
CGGGGCGCCACCTTGCCAGCTCAGGAGTTGGCGGGCATTTACCCCTCAGGATGTGCG
GGCGGAAGTCCGCCCTCTCGCGGCTGAGGGGCGCCCTGAGGGCGAGCACTGGCGTCT

FIGURE 23

MSQFEMDTYAKSHDLMSGFWNACYDMLMSSGQRRQWERAQSRRAQFQELVLEPAQRRARLEGL
 RYTAVLKQQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLKLVN
 HHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELALELTP
 MEAAELDEQREKLVLSAECQLVTVVAVVPGLLEVTTQNVFYFDGSTERVETEEGIGYDFRRP
 LAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTPVSSPSQTPRPQPGPIPPHTQV
 RNQVYSWLLRLRPSPQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQLNTIAGRITYNDL
 SQYPVFPWVLQDYVSPPTLDLSNPAVFRDLSKPIGVVNPKHAQLVREKYESFEDPAGTIDKEH
 YGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDSCDRQFHSVAAAWQARLES PADVKELIP
 EFFYFPDFLENQNGFDLGLCLTNEKVGDVVLPWASSPEDFIQQHRQALESEYVSAHLHEW
 IDLIFGYKQRGPAAEEALNVFYCYTYEGAVDLDHVTDERERKALEGII SNFGQTPCQLLKEP
 HPTRLSAEEAAHRLARLDTNPSIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF
 SFSKDPTMGSHKTPQRLLSGPWPVPGSGVSGQALAVAPDGKLLFSGGHWGSLRVTALPRGKLL
 SQLSCHLDVVTCALADTCGIYLISSGRDTCMVWRLLHQGGLSVGLAPKPVQVLYGHGA AVS
 CVAISTELDMAVSGSEDTGTVIIHTVRRGQFVAALRPLGATFPGPIFHLALGSEGIQVQSSA
 WERPGAQVTYLSHLYSVNGKLRASLPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA
 PPLPMKVAIRSVAVTKERSHVLVGLLEDGKLIVVAGQPSEVRSSQFARKLWRSSRRISQVSS
 GETEYNPTEAR

N-glycosylation site.

amino acids 677-681

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 985-989

Tyrosine kinase phosphorylation site.

amino acids 56-65, 367-376, 543-551

N-myristoylation site.

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,
 873-879, 912-918, 954-960

FIGURE 24

CGGACGCGTGCGGCGGACGCGTGCGGGGCTGTGAGAAAAGTGCCAATAAATACATCATGCAACCC
CACGGCCACCTTGTGAACTCCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCAT
CCAAAGGCCTAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCTGGGGCTCTTC
TGGACCTTAACCTGGGTACTGGCCCTGGGCCAATGCGTCCTCGCTGGAGCCTTTGCCTCCTT
CTACTGGGCCTTCCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCC
GCACACTCCGTTACCACACTGGGTCAATTGGCATTGGAGCCCTCATCTGACCCTTGTGCAG
ATAGCCCGGGTCATCTTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCTGTAGC
CCGCTGCATCATGTGCTGTTTCAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCC
TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAA
AATGCGTTTCATGCTACTCATGCGAAACATTGTGAGGGTGGTCGTCTGGACAAAGTCACAGA
CCTGTGTGTTCTTTGGGAAGCTGCTGGTGGTCGGAGGCGTGGGGGTCTGTCTTCTTTT
TTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAGACTTTAAGAGCCCCACCTCAACTATTAC
TGGCTGCCCATCATGACCTCCATCCTGGGGCCCTATGTTCATCGCCAGCGGCTTCTTCAGCGT
TTTCGGCATGTGTGTGGACACGCTCTTCTCTGCTTCCTGGAAGACCTGGAGCGGAACAACG
GCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGAAC
GAGGCGCCCCCGACAACAAGAAGAGGAAGAAGTGAAGAGCTCCGGCCCTGATCCAGGACTGC
ACCCACCCCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGTCTCCATTTTGTGGT
AAAAAAAGGTTTTAGGCCAGGCGCGGTGGCTCACGCCTGTAATCCAACACTTTGAGAGGCTG
AGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAAATGGTGAACCTCC
GTCTCTATTAAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTATCCCAGCTAC
TCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCGGGAGGCAGAGTTGAGTGAGCCGAGA
TCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAAACAA
AAAGATTTTATTAAAGATATTTGTTAACTC

FIGURE 25

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVGLGF
WTLNWWLALGQCVLAGAFASFYWAFHKPQDIPTFFPLISAFIRTLRYHTGSLAFGALILTLVQ
IARVILEYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAK
NAFMLLMRNIVRVVLDKVTDLLLFFGKLLVVGGVGVLSFFFFSGRIPGLGKDFKSPHLNYY
WLPIMTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMSKSLKILGKKK
EAPPDNKKRKK

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FIGURE 26

GAGTCTTGACCGCCGCCGGGCTCTTGTTACCTCAGCGCAGCGCCAGGCGTCCGGCCGCCGT
 GGCTATGTTCGTGTCCGATTTCCGCAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCC
 TTCTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCT
 CAGTGTGACCACGTGCAATATACGCTGGTTCAGTTCCTGGGTGGCAAGAACTTGAACTGC
 ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAAACTGTGGAGCTAATGTAG
 ACCTATTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGACTCCCATAGG
 CCAGTCAATGTCTCAATGTATACAACGATACCCAGATCAAATTACTCATTAAACAAGATGA
 TGACCTTGAAGTTCCCGCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT
 CAGGAAATGACAGTGATGGGTGAGAGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATA
 GTGGAGCAAACCATGCGGAGGAGGCAGCGCGAGAGTGGGAGGCCCGGAGAAGAGACATCCT
 CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGG
 CTTGGATGCTGTCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC
 CAGTGGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTCGACGG
 CCACGTTTCCCGCCACAACCACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCA
 CACGGATCTCCTTTGAGTATGACCTCCGCCTGGTGCTCTACCAGCACTGGTCCCTCCATGAC
 AGCCTGTGCAACACCAGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA
 GCGGCTCCAGGAGTTCCTTGACAGCATGGGTCTTCCCTGAAAGCAGGTGAAGCAGAAGTCC
 AGGCCATGGACATCTCCTTGAAGGAGAATTTGCGGAAATGATTGAAGAGTCTGCAAATAAA
 TTTGGGATGAAGGACATGCGCGTGACAGCTTTCAGCATTCAATTTGGGTTCAAGCACAAGTT
 TCTGGCCAGCGACGTGGTCTTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCT
 CAGGGACAGATCACTTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG
 TACCATGGCTGGAACCTCGCCAAGAAGCAGCTGCGAGCCACCCAGCAGACCATTGCCAGCTGC
 CTTTGACCAACCTCGTCATCTCCAGGGGCCCTTCTGTACTGCTCTCTCATGGAGGGCAC
 TCCAGATGTGATGCTGTTCTCTAGGCCGGCATCCCTAAGCCTGCTCAGCAAACACCTGCTCA
 AGTCCTTTGTGTGTTGACAAAGAACCGCGCTGCAAACCTGTGCCCCCTGGTGATGGCTGCC
 CCCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGCATCCCCCAGAGACCGACAGCTC
 GGACAGGAAGAACTTTTTGGGAGGGCGTTTGAGAAGGCAGCGGAAAGCACCAGCTCCCGGA
 TGCTGCACAACCATTTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT
 CTGGACGCACTTATTTCCCTCCTGTCCTAGGAAATTTGATTCTTCCAGAATGACCTTCTTATT
 TATGTAACCTGGCTTTCAATTTAGATTGTAAGTTATGGACATGATTGAGATGTAGAAGCCATT
 TTTTATTAAATAAAATGCTTATTTTAGGAAA

GTACCTCAGCGCAGCGCCAGGCGTCCGGCCGCCGTGGCTATGNTCGTGTCCGATTTCCGCA
AAGAGTTCACGAGGTGGTCCAGAGCCAGAGGGTCCTTCTCTTCGTGGCCTCGGANGTGGAT
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAGTGTGACCANGTGCAATATANGCT
GGTTCAGTTTCTGGGTGGCAAGAACTGAAACTGCATTTCTTGAGCATAAAGAACAGTTTC
ATTATTTTATTCTCATAAAGTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT
GAAGACACTATATTCTTGTGTGTGACACCCATAGGCCAGTCAATGTTGTCAATGTATACAA
CGATACCC

FIGURE 29

CAGGAACCCCTCTCTTTGGGTCTGGATTGGGACCCCTTTCCAGTACCATTTTTTCTAGTGAAC
 CACGAAGGGACGATACCAGAAAAACCCCTCAACCCAAAGGAAATAGACTACAGCCCCAATTG
 GCTGACTTTTGGCTATAGAAAAAAGAAAGGAACGAAAGAGACAGTTTTTTTTGGAAAGCTAA
 GTCTTCCCTTTTATCGAGTCAAGAAACCCCCCTTCTTGAGCTATTATACAGCTTTTAACAATT
 GAGTAAAGTACGCTCCGGTACC**CATGGT**GACAGCCGCCCTGGGTGCCCTGGGGCAGCGCTC
 CTGCTCTTTCTCTGATGTGTGATCCGTATGGTGGAGCTCACCTTTGACAGAGCTGTGGC
 CAGCGGCTGCCAACGGTGTGTGACTCTGAGGACCCCTGGATCCTGCCCATGTATCTCTCAG
 CCTCTTCTCCGGCCGCCACGCGCTGCCTGAGATCAGACCCATACATTAAATATCACCATC
 CTGAAGGGTGACAAAGGGGACCCAGGCCAATGGGCCTGCCAGGGTACATGGGCAGGGAGGG
 TCCCCAAGGGGAGCCTGGCCCTCAGGGCAGCAAGGGTGACAAGGGGGAGATGGGCAGCCCCG
 GCGCCCCGTGCCAGAAGCGCTTCTTCGCTTCTCAGTGGGCCCGAAGACGGCCCTGCACAGC
 GCGCAGGACTTCCAGACGCTGCTCTTCGAAAGGGTCTTTGTGAACCTTGATGGGTGCTTTGA
 CATGGCGACCCGCCAGTTTGTCTGCTCCCTGCGTGGCATCTACTTCTTCAGCCTCAATGTGC
 ACAGCTGGAATTACAAGGAGACGTACGTGCACATTATGCATAACCAAGAGGCTGTCTATC
 CTGTACGCGCAGCCAGCCAGCGAGCGCAGCATCATGCAGAGCCAGAGTGTGATGCTGGACCTGGC
 CTACGGGGACCGCGTCTGGGTGCGGCTCTTCAAGCGCCAGCGCGAGAAGGCCATCTACAGCA
 ACGACTTGCACACCTACATCACCTTTCAGCGGCCACCTCATCAGCGCCAGGACGAC**CGA**GGG
 CCTCTGGGCCACCTCCCGGCTGGAGAGCTCAGGTGCTGGTCCCGTCCCTGTCAGGGCTCAG
 TTTGCTACTGCTGTGAAGCAGGAAGGCCAGGGAGGTCCCCGGGGACCTGGCATTCTGGGGAGA
 CCTGCTTCTATCTTGGCTGCCATCATCCCTCCCAGCCTATTCTGCTCCTCTCTCTCTCT
 TGGACCTATTTTAAAGAGCTTGCTTAACTAAATATTCTAAGCCTTCCAGCCTCTGATGCC
 AGCACTTCTCAAACCTTGGAAATGCATGCGAATCACCCGGGTTTCGTGTTAAATGCAGATTCT
 GACTCAGCAGGTCTGAGTGGGTCCAGGATCTGTGTTTCTCATATGTTCTGGGTGATGCTG
 ATGGGGTCAGTCTATGAACCACACTGGAGCAACCAGGTTCTAGGACTTCTCAATATTCTAG
 TACTTTCTGAACATTCTGGAATCCTCCCCACATTCTAGAATTCTCCCAACATTTTTTTTCT
 TGAGACAGAGTCTTGCTCTGTTGCCAGGCTAGAGTGCAGTGGTGCAATCTCAGTTCAGTGC
 AACCTCTGCTCCCGGGTTCAAGCGATTCTTCTGCCTCAGCCTCCCTAGTGGCTGGGATTAC
 AGCGCCTGCTACCATGCTGGCTAATTTTTGTATTTTTAGTAGAGATGGGTTTTACCATA
 TTGGCCAGGCTGCTTGAACCTCTGACTTCAGGTGACCCACCCGCTCGGCCTCTCAAAAT
 GCTGGGATTACAGTGTGAGCCAGGTGCTGGCCAAATTCACCAATTCTTAAATTTCTCAT
 CCTCCAGGGCTCCCCGTGCTATGTTCTCTTTACCCTTCCCCCTCTCTCTTGCTCAGGCC
 TGCACCATGTCAGCCACCGTTCAITTTATTCATTATTAACACTGAGCACTCACTCTGTGCT
 GGGTCCCGGAAGGGTGAGGGGCTCAGACACAGGCCCTGCCCTCAGTCACTGTGCTGCT
 GTCCAGCCAGGCGGGGAGAGATGTGTACATAGGTTTTAAAGCAGACCCAGAGCTCATGGGG
 CCCTGTGTTCTGGGTGTTCAAGTGCTGCTGGTCCCTCCATTCCCACTGCTCCCCAAGGCTGG
 TGGGACGGGTCCCGGTGGCAGGGGAGGTATCTCCTTCCCGTTCTCATCCACCTGCCAG
 TGCTCATCGTTACAGCAAAACCCAGGGGGGCTTGCCAGGTCAAGGGTTCTGTGAGGAGAGG
 ACCCAGGAGTGTGGGGGCTTTGGGGGGTGAAGTGGCCCCGAAGATGGAACCCACACCCA
 TAGCTTCTCCCAAGCTGATACGGCATCTGCGAGAAGACTGCCCTCTCAGCAGTGTGCTGGGATCCC
 CTTCTGCCCTCCTCCAGGCTCTGCCAGGCCTTGCTCAGTCCCTCCCAAGCAAGTCACTCT
 GAACCTCCGTTTCCCCAGGGCTCCAGCTGCCCTCAGACACTGATGTCTGTCCCCAGGTGCT
 CTCTGCCCTCATGCCCTCTACCGCCCACTGCCCCGACTCTCCAGGCTTTATCAAGGTG
 CTAAGGCCCGGGTGGGCAGGTCCTCGTCTCAGAGCCCTCCTCCGGCTGGTGTGCTGCTTAC
 AAACACCTGCAGGAGAAGGGCCACGGAAGCCCCAGGCTTTAGAGCCCTCAGCAGGTCTGGGG
 AGGTAGAGCAAAAGGAGGACCTCAGGCCTTCCGTTTCTTCTCCAGGGTGGGGTGGGCTGGT
 GTTCCCTAGCCTTCCAAACCCAGTGGCCTGCCCTTCTCCCAAGAGGGAGGCGCTCCGC
 CCATTGGTGCTCATGCAGACTCTGGGGCTGAGGTGCCCGGGGGGTGATCTGGTGCTCAC
 AGCCGAGGGAGCCGTGGCTCCATGGCCAGATGACGGAACAGGGTCTGACCAAGTGCACGA
 AGACCTGTGCTATAAACACCCCTGCCTGATCTGCCCTGCCTGACCCCGCCACGCCCTGCC
 GTCCAGCATGATTAAGAATGCTGTCTCTTGGAAAAA

FIGURE 30

MVTAALGPVWAALLLFLLMCEIRMVELTFDRAVASGCQRCCDSEDLDPAHVSSASSSSGRPH
ALPEIRPYINITILKGDGDPGPMGLPGYMGREGPQGE PGPQGSKDGKGMGSPGAPCQKRF
FAFSVGRKTALHSGEDFQTLLEFVFNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET
YVHIMHNQKEAVILYAQPSESRIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYIT
FSGHLIKAEDD

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation site.

amino acids 72-75

Clq domain proteins.

amino acids 144-178, 78-111 and 84-117

FIGURE 31

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGACCCGCCAGGAAAGACTG
 AGGCCGCGGGCTGCCCGGCCGGCTCCCTGCGCCGCCCGCCCTCCCGGGACAGAAGATGTG
 CTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCTGGGGTGCAGG
 GCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGCTTTCTGCACCTGCTCCCGCAGGGG
 ACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTACGCTCTTTGAGAACGGCAT
 CACCATGCTCGACGCAGGCAGCTTTGCGCGGCTGCCGGGCTGCAGCTCCTGGACCTGTAC
 AGAACAGATCGCCAGCCTGCCAGCGGGTCTTCCAGCCACTCGCCAACTCAGCAACCTG
 GACCTGACGGCCAACAGGCTGCATGAAATACCAATGAGACCTTCCGTGGCTGCGGCGCT
 CGAGCGCTCTACCTGGGCAAGAACCGCATCCGCCACATCCAGCCTGGTGCTTCGACACGC
 TCGACCGCTCCTGGAGCTCAAGCTGCAGGACAACGAGCTGCGGGCACTGCCCCCGCTGCGC
 CTGCCCCGCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCGGCAT
 CCTGGACACTGCCAAGCTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACG
 AGGGGCTCTTCAGCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGACAACAGCTGGAG
 CGAGTGCCACTGTGATCCGAGGCTCCGGGGCTGACGCGCTGCGGCTGGCCGGCAACAC
 CCGCATTGCCAGCTGCGGGCCGAGGACCTGGCCGGCTGGCTGCCCTGCAGGAGCTGGATG
 TGAGCAACCTAAGCTGCAGGCCCTGCCTGGCGACCTCTCGGGCTCTTCCCCCGCTGCGG
 CTGCTGGCAGCTGCCGCAACCCCTTCAACTGCGTGTGCCCTGAGCTGGTTGGCCCTG
 GGTGCGCGAGAGCCACGTGCACACTGGCCAGCCCTGAGGAGACGCGCTGCCACTTCCCGCCA
 AGAAGCTGCGCGGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGCTGCCAGCCACCAACC
 ACCACAGCCACAGTGCCCAACACGAGGCGCGTGGTGCGGGAGCCACAGCCTTGCTTCTAG
 CTGGGCTCTTACCTGGCTTAGCCCCACAGCGCCGGCCACTGAGGCCCCAGCCGCGCTTCCA
 CTGCCCCACCGACTGTAGGGCTGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCTC
 AATGGGGGCACATGCCACCTGGGGACACGGCACCACTGGCGTGCTGTGTCCCGAAGGCTT
 CACGGCCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCCTACACAGTCA
 CGCCGAGGCCACCACGGTCCCTGACCTGGGCATCGAGCCGCTGAGCCCCACCTCCCTGCGC
 GTGGGGCTGCAGCGTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTA
 TCGCAACCTATCGGGCCCTGATAAGCGGCTGGTGACGCTGCGACTGCGCTCCTCGCTCGGTG
 AGTACACGGTCACCCAGCTGCGGCCAACGCCACTTACTCCGTCTGTGTATGCCCTTGGGG
 CCGGGCGGGTGCCGGAGGGCGAGGAGGCTGCGGGGAGGGCCATACACCCAGCCGCTCCA
 CTCCAACACAGCCCCAGTACCCAGGCCCGCAGGGCAACCTGCCGCTCCTCATTTGCGCCG
 CCTGCGCGGGTGCTCCTGGCCGCGCTGGCTGCGGTGGGGGAGCCTACTGTGTGCGGCGG
 GGGCGGGCCATGGCAGCAGCGGCTCAGGACAAAGGCGAGTGGGGCAGGGGCTGGGCCCT
 GGAAGTGGAGGGAGTGAAGTCCCTTTGGAGCCAGGCCGAGGCAACAGAGGGCGGTGGAG
 AGGCCCTGCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCAGGGCTGGCCTC
 CAGTACCCCTCCAGCCAAAGCCCTACATCTAAGCCAGAGAGACAGGGCAGCTGGGGCCG
 GGCTCTCAGCCAGTGAGATGGCCAGCCCTCCTGCTGCCACACCAGTAAAGTTCTCAGTCC
 CAACCTCGGGGATGTGTGCAGACAGGCTGTGTGACCAAGCTGGGCCCTGTTCCCTCTGGA
 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAAC
 CGAGTGCCATATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCG
 GGCCCTGCCATGTGCTGGTAACGCATGCTGGGTCTGCTGGGCTCTCCACTCCAGGCGGA
 CCTGGGGGCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGCTAGGCGGCTGTG
 TGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGCTTTA
 GGAACATGTTTTGCTTTTTTAAATATATATATTATAAGAGATCTTTCCACTTTATCTG
 GGAAGATGTTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTAAAGACAAACGATGATAG
 AAGGCCTTTTGTAAAGAAAAATAAAAGATGAAGTGTGAAA

FIGURE 32

MCSRVPLLLLPLLLLLLAGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPDPTVGLYVFEN
GITMLDAGSFAGLPGLQLLDLSQNIQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLR
RLRLYLKGNRIHIQPGAFDTLDRLLELKLQDNELRALPLRLPRLLLLDLSHNSLLALEP
GILDTANVEALRLAGLGLQQLDEGLFSRLRNLDLHLDVSDNQLERVPPVIRGLRGLTRLRLAG
NTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDSLGLFPRLLRLAAARNPFNCVCLPSWFG
PWVRESHVTLASPEETRCHFPKKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALS
SSLAPTWLSPTAPATEAPSPSTAPPTVGVPVQPQDCPSTCLNGGTCHLGRHHLACLCE
GFTGLYCESQMGGTRPSPTVTPRPPRSLTGIEPVSPSTSLRVGLQRYLQGSSVQLRSRL
TYRNLSPDKRLVTLRLPASLAEYTVTQLRPNATYSVCMPLGPGRVPEGEEACEGAHTPPA
VHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRAMAAAAQDKQVGPAG
PLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPHLAKPYI

FIGURE 33

GAATCATCCACGCACCTGCGAGCTCTGCTGAGAGAGTGCAAGCCGTGGGGGTTTTGAGCTCAT
 CTTTCATCATTCATATGAGGAAATAGTGGTAAAACTCCTTGGGAAATAC**AATG**AGACTCATCAG
 AAACATTTACATATTTTGTAGTATTTGTTATGACAGCAGAGGGTGATGCTCCAGAGCTGCCAG
 AAGAAAGGGAAGTATGACCAACTGCTCCAACTATGCTCTAAGAAAGGTTCGCCGAGACTTG
 ACCCCAGCCACAACGACACTGGATTTATCCTATAACCTCCTTTTCAACTCCAGAGTTGAGA
 TTTTCATTTCTGCTCCAACTGAGAGTTTGTATCTATGCCATAACAGAAATCAACAGCTGG
 ATCTCAAAACCTTTGAATTCACACAGGAGTTAAGATATTTAGATTTGTCTAATAACAGACTG
 AAGAGTGTAACCTTGGTATTACTGGCAGGCTCAGGTATTTAGATCTTTCTTTTAATGACTT
 TGACACCATGCTATCTGTGAGGAAGCTGGCAACATGTACACCTGGAAATCCTAGGTTTGA
 GTGGGGCAAAAATACAAAATCAGATTTCCAGAAAATTTGCTCATCTGCATCTAAATACGTCT
 TTCTTAGGATTCAGAACTCTTCTCATTATGAAGAAGGTAGCCTGCCCATCTTAAACACAAAC
 AAAACTGCGACATTTGTTTACCAATGGACACAAAATTTCTGGGTTCTTTTGGCGTATGGAATCA
 AGACTTCAAAAATATTAGAATGACAAATATAGATGGCAAAAGCCAATTTGTAGTTATGAA
 ATGCAACGAAATCTAGTTTGAAGAAATGCTAAGACATCGGTTCTATTGCTTAATAAAGTTGA
 TTTACTCTGGGACGACCTTTTCTCTATCTTACAATTTGTTTGGCATAACATCAGTGGAAACAT
 TTTAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAAATTCATTTGACTAC
 TCAAAATAGTAAATGAGAACTATAAAAATTGGAGCATGTACATTTAGAGTGTTTTACATTTCA
 ACAGGATAAAAATCTATTTGCTTTTGACCAAAATGGACATAGAAAACCTGACAATATCAAAAT
 CAGAAATGCCACACATGCTTTTCCCGAATTTATCTACGAAATTTCAAATTTTAAATTTTGGC
 AATAATATCTTAAACAGACAGTTGTTTAAAGAAGTATCCAAGTGGCTCAGCTTGAAGAACTCT
 CATTTTGAATGGCAATAAGACTGGAGACACTTTCTTTAGTAAGTTGCTTTGTCAACACACAC
 CCTTGGAAACACTTGGATCTGAGTCAAAATCTATTACAACATAAAAATGATGAAAATTTGCTCA
 TGGCCAGAACTGTGGTCAATATGAATCTGTCTATACAATAAATTTGCTGATCTGTCTCAG
 GTGCTTGGCCAAAAGTATTCAAATACCTTGACCTTAAATAAATCAACCAATCCAACTGTACCTA
 AAGAGACTATTCATCTGATGGCCCTTACGAGAACATAATTTGCATTTAAATTTTCTAATGAT
 CTCCCTGGATGCAGTCAATTTAGTAGACTTTTCAAGTCTGAACATTTGAATGAATCTTATCT
 CAGCCCATCTCTGATTTTGTTCAGAGCTGCCAGGAAGTTAAACACTTAAATCGGGGGAAGAA
 ATCCATCTCGGTGACTCTCCACGAATTTTCAATGAGCTTTGAACACATATTACAGAGGTC
 ATGATGGTTGGATGGTCAGATTATACACCTGTGAATACCCCTTAAACCTAAGGGGAACATAG
 GTTAAAGAGCTTATCTCTCCACGAATTTCTTGCAACACAGCTGTGTTGATTGTCCACATTG
 TGGTTATTATGCTAGTTCTGGGGTTGGCTGTGGCTTCTGCTCTGCCATTTGATCTGCC
 TGGTATCTCAGGATGCTAGGTCAATGTCACACAAACATGGCACAGGTTTAGGAAAACACCCA
 AGAACAACTCAAGAGAAATGTCGGATTCCACGCATTTATTTTCATACAGTGAACATGATCTC
 TGTGGGTGAAGAAATGAATGTATGCCCAATCTAGAGAAGGAAGATGGTCTATCTTGTATTGCT
 CTTTATGAAGCTACTTTTGACCTTGGCAAAAGCATTAGTGGAAGAAATATTGAGCTCTATTGA
 GAAAAGCTATAAGTCCATCTTTGTTTGTCTCCCACTTTGTCCAGAAATGAGTGGTGGCATT
 ATGAATTTCAATTTGGCCACCACAATCTCTCCATGAAAATCTGATCATATAATTTCTATC
 TTACTGGAACCCATTCCATTTCTATTGCAATTTCCACCAGGTATCATAACTGAAAGCTCTCTCT
 GGAAAAAAGCACTACTTTGGAATGGCCCAAGGATAGGCGTAAATGTGGGCTTTTCTGGGCAA
 ACCCTTCGAGCTGCTATTAATGTTAATGTATTAGCCACCAGAGAAATGTATGAAGTGCAGACA
 TTCACAGAGTTAAATGAAGAGTCTCGAGGTTCTACAATCTCTGATGAGAACAGATTGTCT
ATAAAATCCACAGTCCTTGGGAAGTTGGGGACCACATACACTGTTGGGATGTATACATTGATA
 CAACCTTTATGATGGCAATTTGACAATATTTATTAATAAAAAAATGGTTATTCCTTCATA
 TCAAGTTTATGAGAGGATTTCTAGAAGATGATCTTATGAAACACCTTCACAAGTTTATAAGG
 GCTTATGGAAGAAAGGTTCATCCACAGGATTTGTTATAATCTAGAAAATGTGGCCAGGTGCA
 AGTGGCTCACTCTTGTAATCCCAAGCATATGGGAGGCCAAGGTGGGTGACCCAGAGGTCAA
 GAGATGGAGACCATTCTGGCCAACATGGTGAACCCCTGTCTACTATAAAATACAAAAATTA
 GCTGGGCGTGATGGTGCAGCCTGTAGTCCCAGCTACTTGGGAGCTGGAGCGAGAGAATCG
 CTTGAACCCGGGAGGTGGCAGTTGCAGTGAGCTGAGATCGAGGCCACTGCACTCCAGCCTGGT
 GACAGAGCGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAAATGAAAAACATCC
 TCAATGGCCACAAAATAAGTCTAATTCATAAAATATAGATACATTAATGTAAATATAATTA
 CATGCCACTAAAAAGAATAAGGTAGCTGTATATTTCTGGTATGGAAGAAAAACATATTAATTA
 GTTATAAATCTATTAGGTTGGTGCAAAATTAATTTGTGGTTTTTGGCATTGAAATGGCATTGAA
 ATAAAGTGTAAAGAAATCTATACCAGATGTAGTAACAGTGGTTTGGGTCTGGGAGGTTGGA
 TTACAGGAGCATTTGATTTCTATGTTGTGTATTTCTATAATGTTTGAATTTGTTAGAATGA
 ATCTGTATTTCTTTTATAAGTAGAAAAAATTAAGATAGTTTTTACAGCTT

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FIGURE 34

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLT PATTTLDLSYNLLFQ
LQSSDFHVSVKLRVLILCHNRIQQDLKTFEFNKELRYLDLSNNRLKSVTWYLLAGLRYLDL
SFNDFDTPICEEAGNMSHLEILGLSGAKIQKSDFKIAHLHLNTVFLGFRTLPHYEEGSLP
ILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL
LNKVDLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
VFYIQQDKIYLLLTkMDIENLTISNAQMPHMLFPNYPTKFQYLN FANNILTDELFKRTIQLP
HLKTLILNGNKLETLSLVSCFANNTPLEHLDLSONLLQHKNDENCSWPETVVNMNLSYNKLS
DSVFRCLPKSIQILD LNNNQITVPKETIHLMALRELNIAFNFLTDLP GCSHFSRLSVLNIE
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLETYSEVMVMGVSDSYTCEYPLN
LRGTRLKDVHLHELSCNTALLIVTIVVIMLVGLAVAFCC LHFDLFPWYLRMLGQCTQTWHRV
RKTQEQQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENI
VSFIEKSYKSI FVLSPNFVQNEWCHYEFYFAHNL FHENS DHIILILLEPIPFYCIPTRYHK
LKALLEKKAYLEWPKDRRKCGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLM
RTDCL

FIGURE 35

GGGGGCTTTCTGGGCTTGGCTGCTTGAACACCTGCCTCCAAGGACCGGCTCGGAGGGGTGCGCGGGAAAGG
 GAGGGAAGAGGAGGGCGGGGCGGGCCCCCTGCGCGCGCGCGCGCTCTGCGCGCGCTGTCCGCGCGCGG
 CAGGCCAGCCCGAGCCCGCGGGCGGGTCAACGCGCAGCCAGCGCGCGCTCCGCGCGCGCGCGCGCT
 CTGCTGTGCCCTGCGCCCTTGCCCCGCGCAGCTTCTGCGCGCGCAGCCCGCGCGCGCGCGCGGTGACCGTGA
 CCTCGCCCTGGGCGCGGGCGGGAGCAGGCATGCTCCCGCGCGGGGACCGCTACCCGACCGCTGGGCCCTGGTGCCT
 CTGGCAGTGACCTGCGCGGGGTGCGAGCCCGAGGCGCAGCCCTCGAGGACCGCTGATTATTACGGGCGAGGAGAT
 CTGGAGCGGGAGCCCTACTACGCGCGCGCGGAGCCGAGCTCGAGACCTTCTCTCCGCGCGCTGCTGCGGGGCG
 CCGGGGAGGAGTGGGAGCGGCGCGCGCAGGAGCCCGAGCGCGCCCAAGAGGGGCCACCAAGCCCAAGAAAGCTCCC
 AAGAGGGAGAAGTCGGCTCGGAGCGCGCTCCACCAGGTAAACACAGCAACAAAAAGTTATGAGAACCAGAG
 CTTCTGAGAAGGCTGCCAACGATGATCAGCTGTCGCTGCGCCGCTGAAGATGTCAGAGAGATGTGCCACCTC
 TTGGTCTGGAACCTTAAAAATCACAGACTTCAGCTCCATGCCTCCACGGTGAAGCGCTATGGCTGGGGGCA
 CATCGAGGGAGACTCAACATCCAGCGGGCATTAATGAAATGATTTTATGACGGAGCGTGGTGCAGCGGAAG
 AATGACCTCCAGCAGTGGATTGAAGTGGATGCTCGGCGCTGACGAGATTCACTGGTGTCACTCAAGGGA
 GGAACCTCCTCTGGCTGAGTGACTGGGTGACATCCTATAAGGTCMTGGTGAGCAATGACAGCCACAGCTGGGTG
 ACTGTTAAGAATGGATCTGGAGACATGATATTTGAGGGAACAGTGAAGAAGGAGATCCCTGTTCTCAATGAGCT
 ACCCGTCCCATGGTGGGCGGCTACATCCGCATAAACCTCAGTCTGTTTGAATAATGGGAGCATCTGCTATGA
 GAATGGAGATCTGGGCTGCCACTGCCAGATCCTAATATTATTTATCAGCGCGGAACGAGATGACCCACT
 GTAGCTGGATTGTTAAGCACCACAAATATAAGGAAATGCGCCAGTTGATGAAGTTGTGAATGAATGTTGTC
 CAATATCACCAGAAATTAACAATTTGGAAGAGCCAGCGGGCTGAAGCTGTATGCTGTGGAGATCTCAGATG
 ACCCTGGGAGCATGAAGTCGGTGAGCGCGAGTTCCACTACATCGCGGGGCGCCACGGCAATGAGGTGCTGGG
 CGGAGCTGCTGCTGCTGCTGGTGAGTTCGTGTGTCAGGAGTACTTGGCCCGGAATGCGCGCATGCTGCCACT
 GGTGGAGGAGACCGGATTACGCTGCTCCCTCCCTCAACCCGATGGGTACGAGAAGGCTACGAGAGGCGCT
 CGGAGCTGGGAGCTGGTCCCTGGGAGCTGGAGCCACGATGGAATTGACATCAACAACAACCTTCTCTGATTTA
 AACACGCTGCTCTGGGAGGCGAGGATCGACAGAATGTCCCCAGGAAAGTTCCCAATCACTATATTGCAATCCC
 TGAGTGGTTCTGTGGAAATGTCAGCGGTGGCTGCGGAGACCAGAGCATGCTAGCTGCGTGGGAAATAATCC
 CTTTTGTGCTGGCGGCAACCTGCAGGCGCGCGAGCTGGTGGTGGCTATCCCTACGACCTGGTGGCGTCCCC
 TGAAGACGCGAGGAACACACCCCCACCCCGATGACCAGTGTTCGCTGGCTGGCTACTCCTATGCGCTCCAC
 ACACCGCTCATGACAGACGCCCCGAGGAGGTTGCCACACGAGGAGCTCCAGAAGGAGGAGGCGACTGTCA
 ATGGGCGCTCCTGGCACACCGTGGTGGAAAGTCTGAACGATTTCACTACCTTCATACAAATGCTTCCAATG
 TCCATCTACCTGGGCTGTGATAAATACCCACATGAGAGCGAGCTGCCGAGGAGTGGGAGAAATACCGGGAATC
 TCTGATCGTGTCAATGGAGCAGGTTTCATCTGGCATTAAAGGCTTGGTGAGAGATTCACTGGAAGGAATCC
 CAAACGCCATTATCTCCGTAGAAGGCATTAAACATGACATCCGAACAGCCAAACGATGGGGAATCTGGCGCGCTC
 CTGAACCTCGAGAGTATGTGTGTCAGCAAGAGCCGAAGGTTTCACTGCATCCCAAGAACTGTATGGTTGG
 CTATGACATGGGGGCCACAAGTGTGACTTCACACTTAGCAAAACCAAGTCCGAGGATCCGAGGATCATGG
 AGAAGTTTGGGAAGCAGCCGCTGAGCTGCCAGCCAGGCGGTGAAGCTGCGGGGCGGAAGAGACGACAGCGCT
 GGCTGACCTCTGGGCGCTTGAGACTGCTGGGACCCATGCAAAATTAACCAACCTGGTAGTAGTCCATAG
 TGGACTCACTCACTGTTGTTTCTCTGTAATTCAAGAAGTGCTGGAAGAGAGGCTGCAATTGTGAGGCGAGTCC
 CAAAGGGGAAGGCTGGAGGCTGAGGCTGTTTTCTTTCTTTGTTGCCATTTATCCAATAACTTGGACAGAGCA
 GCAGAAAGAGCTGATGGGAGTGAGAGAATCAGCAAGCCAACTGGGAATCAGAGAGAGAAGGAGAAGGAGG
 GAGCCTGTCCGTTAGAGCCTCTGGCTGCATAGAAAGGATTCTGGTGCTTCCCCTGTTTGGCTGGCAGCAAGG
 GTTCCACGTGCAATTTGCAATTTGCAAGTTTCAAAATTCAGCATTTCGCCAGTGGGCTGTCCTCAATGTTTACCA
 TTTGAGATGCTCCAGGCGCTCCTAAGAGAAATCCACCTCTCTGGCCCTGGGACATGCAAGCTGCTACAAATTA
 ATTCTGTGTTCTTTGACAATAGGCTCATTTGCCAAGTGCACATCAGTGAAGCTCTTGAATCTGTTGAATCTT
 TTTTCAACARAGGAGTGTGTTGAGAAAAGGAGAGAGGCTGAGATCATTCAAGGAGTTTGTGGGCGAGCAAGCA
 TGGAGCTTCTGCACAAATTTGGGTCATAAACACCCCAAGTCCCTGCTGATCCAGTAGCCCTGGAGGTT
 CCCAGCTAGGGAAGCCAGAGGTTGCCAGCTTCCGTAAGGGCCAGAAAATTTAGCTGGATCTCCTGATCTCCTTAC
 CTGCTAGGACTCGAAAGAGCCAGAAGTGGGCTGGCTGAAGCCCTCTCTGCTTGAAGTATTGCCCTGTGCTGA
 GAATGAGTGCTCATGGGTGGCCCTCATATCAGCTGGGAGTTATTTTATATGATGATGATGATGATGATGATGAT
 GATTAGGCTAAATGTAATGAAACCTCTTAGGATTATCTGTGGAGCATCAGTTTGGGAAGAAATTTATGAAATTA
 CTGCAAGAAAAAGTATGCTCACTCTTTTGTAAATGTTGCTGCCTCACTGACCTGGGAAAGTAAAAA
 AATAAAGCAAAATGTAAGACCTTAAAAA

FIGURE 36

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPPYARPEPELETFSPLP
AGPGEEWERRPQEP RPPK RATKPKKAPKREKSAPEPPP GKHSNKKVMRTKSSEKAANDDHS
VRVAREDVRESC PPLGLETLKITDFQLHASTVKRYGLGAHRGR LNIQAGINENDFYDGAWCA
GRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSND SHTWVTVKNGSGDMIF
EGNSEKEIPVLNELPVPMVARYIRINPQSWFDNGSICMRMEILGCPLPD PNNYYHRRNEMTT
TDDLDFKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEF
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLPSLNP DGYEKAYEGG
SELGGWSLGRWTHD GIDINNNFPDLNTLLWEAEDRQNVPRKVPNH YIAIPEWFLSENATVAA
ETRAVIAWMEKIPFVLGGNLQGGELVVAYPYDLVRSPWK TQEHTPTPDDHVFRWLAYSYAST
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFS YLHTNCFELSIYVGCDKYPHES
QLPEEWENNRESLIVFMEQVHRGIKGLVRDSHGKIPNAIISVEGINHD IRTANDGDYWRLL
NPGEYVVTAKAEGFTASTKNCMVG YDMGATRCDFTL SKTNMARIREIMEKFGKQPVSLPARR
LKLGRKR RQRG

FIGURE 37

CTAAGAGGACAAGATGAGGCCCGCGCCTCTCATTTCTCTAGCCCTTCTGTCTCTTCTGGCCAAAGCTGCAGGGG
 ATTTGGGGGATGTGGGACCTCCAATTCAGCCCGCGCTTCAGCTCTTTCCAGGTGTGACTCCAGCTCCAGC
 TTCAGCTCCAGCTCCAGGTTCGGGCTCCAGCTCCAGCCGCGAGCTTAGGCAGCGGGAGTTCTGTGTCCAGTTGTT
 TTCCAATTTACCGGCTCCGTGGATGACCGTGGGACCTGCCAGTGCTCTGTCTCCCTGCCAGACACCACTTTTC
 CCGTGGACAGATGGGAACGCTTGGAAATTCAGAGCTCATGTTCTTTCTCAGAAGTTTGAGAAGAACTTTCTAAA
 GTGAGGGAATATGTCCAATTAATAGTGTGTATGAAAAGAACTGTTAAACCTAACTGTCCGAATTCACATCAT
 GGAGAAGGATACCATTTCTTACACTGAACCTGGACTTCGAGCTGATCAAGGTAGAAGTGAAGGAGATGGAAAAAC
 TGGTCATACAGCTGAAGGAGAGTTTTGGTGAAGCTCAGAAATTTGTGACCAGCTGGAGGTGGAGATAAGAAAT
 ATGACTCTCTTGGTAGAAGAGCTTGAGACACTAGACAAAACAATGCTCTTGCCATTGCGCGAGAATCGTGGC
 TCTGAAGACCAAGCTGAAGAGTGTGAGGCTCTAAGATCAAAACACCCCTGTGCTGCCACCTCTCTCCCACTC
 CAGGGAGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAAACCGTCTGTGGTTGAGCTCAACTGGAGAGGGTTT
 TCTTATCTATATGGTGCTTTGGGTAGGGATTACTCTCCCCAGCATCCAAACAAAGGACTGTATTGGGTGGCGCC
 ATTTGAATACAGATGGGAGACTGTTGGAGTATTAAGACTGTACAACACACTGGATGATTGCTATTGTATATAA
 ATGCTCGAGAGTTGCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACACATGTACGTCAAC
 ATGTACAACACCGGGAATATTGCCAGAGTTAACTGACCACCAACAGATTGCTGTGACTCAAACCTCTCCCTAA
 TGCTGCCTATAATAACCGCTTTTCATATGCTAATGTTGCTTGGCAAGATATTGACTTTGCTGTGGATGAGAATG
 GATTGTGGGTTATTTATTTCACTGAAGCCAGCACTGGTAACATGGTGATTAGTAAACTCAATGACACCACACTT
 CAGGTGCTAAACACTTGGTATACCAAGCAGTATAAACCATCTGCTTCTAACGCTTCATGGTATGTGGGGTTCT
 GTATGCCACCCGTACTATGAACACCAGAACAGAAAGAGATTTTTTACTATTATGACACAAACACAGGGAAAGAGG
 GCAAACTAGACATTGTAATGCATAAGATGCAGGAAAAAGTGCAGAGCATTTAACTATAACCCCTTTTGACCAGAAA
 CTTTATGTCTATAACGATGGTTACCTTCTGAATATGATCTTTCTGTCTTGCAAGAGCCCCAGTAAAGCTGTTTA
 GGACTTAGGTTGAAGAGAAAAATGTTTGTGAAAAATAGTCTTCTCCACTTACTTAGATATCTGCAGGGGTGT
 CTAAGAGTGTGTTCAATTTGCGAGCAATGTTTAGTGTCATAGTCTTACCACACTAGAGATCTAGGACATTTGTCT
 TGATTTGGTGAGTTCTCTTGGGAATCATCTGCCTCTTCAGGCGCATTTTGCATAAAGTCTGTCTAGGGTGGGA
 TTGTGAGAGGTCTAGGGGCACTGTGGGCTTAGTGAAGCCTACTGTGAGGAGGCTTCACTAGAAGCCTTAAATTA
 GGAATTAAGAACTTAAAACTCAGTATGGCGCTAGGGATTCTTTGTACAGGAAATATTGCCAATGACTAGTC
 CTCATCCATGTAGCACCCTAATTTCTTCCATGCCGGAAGAAACCTGGGGACTTAGTTAGGTAGATTAATATCT
 GGAGCTCCTCGAGGGACCAATCTCCAACCTTTTTTCCCTCACTAGCACCTGGAAATGATGCTTTGTATGTGG
 CAGATAAGTAAATTTGGCATGCTTATATATTCTACATCTGTAAAGTGTGAGTTTTATGGAGAGAGCCCTTTT
 ATGCATTAATTTGTACATGGCAATTAATCCAGAAGGATCTGTAGATGAGGCACCTGCTTTTCTTTTCTCTC
 ATTGTCCACCTTACTAAAAGTCAGTAGAATCTTCTACCTCATAACTTCTCTCCAAAGGCAGCTCAGAAGATTAG
 AACCAGACTTACTAACCAATTCACCCCCACCAACCCCTTCTACTGCCACTTTAAAAAATTAATAGTTTT
 CTATGGAATGATCTAAGATTAGAAAAATTAATTTTCTTTAAATTTCAATATGGACTTTTATTTACATGACTCTA
 AGACTATAAGAAAACTGATGGCAGTGACAAAGTGTAGCATTTATTTGTTATCTAATAAAGACCTTGGAGCATA
 TGTGCAACTTATGAGTGTATCAGTTGTGCATGTAATTTTGCCTTTGTTTAAAGCCTGGAACCTTGTAAAGAAAT
 GAAAATTTAAATTTTTTTTCTAGGACGAGCTATAGAAAAGCTATTGAGAGTATCTAGTTAATCAGTGCAGTAGT
 TGGAAACCTTGTGTTGTATGTGATGTGCTTCTGTGCTTTTGAATGACTTTATCATCTAGTCTTTGTCTATTTT
 TCCTTTGATGTTCAAGTCCTAGTCTATAGGATTGGCAGTTAAATGCTTTACTCCCCCTTTTAAAAATAATGAT
 TAAAAATGTCCTTTGAAAAAAGAAAAAAGAAAAAAGAAAAA

MRPGLSFLLLALLFFLQGAAGLDGVDGPPIPSPGFSFSPGVDSSSSFSSSSRSGSSSSRLGS
GGSVSQLFSNFTGSDRGTQCQSVSLPDTTFPVDRVERLEFTAHVLSQKFEKELSKVREYV
QLISVYEKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ
LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALKTKLKECEASKDQNTPVVHPPTPGSCGH
GGVNVISKPSVVQLNWRGFSYLYGAWGRDYSQHPNKGLYWVAPLNTDGRLLLEYRLYNTLD
DLLLYINARELRITYQGSGTAVYNNNMVNMNTGNIARVNLTNTIAVTQTLPNAAAYNNR
FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDDTLQVLNTWYTKQYKPSASNAF
MVCGLYATRMTNTRTEEIFYYDNTNGKEGKLDIVMHKMQEKVQSINYNPFQKLYVYNDG
YLLNYDLSVLQKPO

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FIGURE 39

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAACACCCCTGTCGTCCAC
CCTCCTCCCACTCCAGGGAGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGT
GGTTCAGCTCAACTGGAGAGGGTTTTCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTC
CCCAGCATCCAAACAAAGGNATGTATTGGGNGGCGCCATTGAATACAGATGGGAGACTGTTG
GAGTATTATAGACTGTACAACCCACTGGATGATTTGCTATTGTATATAAATGCTCGAGAGTT
GCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAACA
TGTACAACACCGGNATATTGCCAGAGTTAACCTGACC

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAACACCCCTGTCGTCCAC

TCTCGCAGATAGTAAATAATCTCGGAAAGCGGAAAGAAAGCTGTCTCCATCTTGTCTGATAT
 CCGCTGCTCTTTGTGACGTTGTGACAGCATGGGAGCGCTCTGGGGCTGTGCTCATGTCGCAGT
 GGAATACCATGTTTGTGTGGAAAGTGGCCCGTGTTTGCTATGCCGATGCTGTCTAGTGGAAAC
 AACTCCATCTGTAATCAGTATGATATGACCACTTTCTTGCTTGTGGAGTATGTTGAGCTTGT
 TGTAAATGTTGATACCGAGGAATGGAAGAACAACTGAATAAGATTTCCCTGGATTTGTGAAATGT
 AGAAAGGTGTTGTGCCCTTTGTAACATTTTGGTGTGCGTATAAAGCTGTATATCGTTTGTGCTTT
 TTTTGGGTATGTTTCTATCTTCTTCTCTTACTAATGATCAAAAGTGAAGACGTAGCAGTGA
 TCTTAGAGTCTCGAGTGCACAATGGATTTTGGTTCTTTAAATTTGCTGCGACGAATTGCAATTA
 TTAATTTGGGCACTTCTTCAATCCGAAGGAACCTTTACAACCTGTGTGGTTTATGTAGGACGT
 CGAGGTGCCTTTGTCTTCACTCTCATCAACTAGCTCTTACTTATTGATTTTGACATTCATG
 GAATGAATCGTGGGTTGAAAAAATGAAGAAGGAACGTGAGATGTGGTATGCGACCTTTGT
 TATCAGCTACAGCTCTGAATTTATCTGCTGTCTTTAGTTGCTATCGTCTCTGTTCTTTGCTCTAC
 TACACTCATCCAGCGAGTGTTTGAGAAAAACAAGGCGTTCATCAGTGTCAACATGCTCTCTCG
 CGTTGGTGCTCTGTAATGTCTATACTGCCAAAACTCAAGAATCAACAACCAAGATCTGTGTT
 TGTTACAGTCTTTCAGTAATTACAGTGTACACAATGTAATTTGACATGTGCAGTATGACCAAT
 GAACCAAGAACAAATTCGAACCCAAGCTTACTAAGCATTAATTTGGCTACATAACAACAGCAC
 TGTCCCAAGAGGAGGGCGATTCAGTCAGTGGTGGCATGCTCAAGGAATTAAGGACATAATCT
 TCTTTTGTGTGGTGATTTTATTTCCAGCATCGGTACTTCAACAATAGTCAGGTAAATTAAC
 CTGACTCTAACAAGTGAATGATATTAATAGAAATGTTGGAGCTAGAAGTGAATGATGATC
 ACTGAGAGATGGGACGATGTTACCAGAGCTAGATAGTAAGAAAGGATGGTGTCATTTACA
 GTTATCTCTTCTTCACTTACGTCTTTCTGGCTCACTTTATATCATGATGACCTTACC
 AACTGGTCCAGGTATGACCTCTCGTGAGATGAAAGCTCAGTGGACAGTCTGGGTGAA
 AATCTCTTCCAGTTGGATTGGCATCGTGCTGTATGTTTGGCACTCGTGGCACTTGTGTT
 TACAAATCGTGAATTTGACGTAGAGACTCTAGCATGAAAGTCCCACTTTGATTTATGCT
 TTAATTTGAAAAAGTATTTCCAACCTTTTGTAAAGTGTGATATGTTTGTCTCCCATGTAA
 TCTCCAGTGTTCTGGCATGAATTGATATTTACTGCTTGTCATTTGTGTATTTCTTACCAAG
 GTGCATTGATATGTGAAGTAGAATGAATTCGAGAGGAAAGTTTATGAATATGGTGATGAGT
 TAGTAAAGGTGGCCATTTGGGCTTATTTCTGCTCTATAGTGTGAAATGAAGAGTAAAA
 ACAAATTTGTTTGACATTTTAAATATTTATGACCTTAAGCTGTTTTAGCAGACATTAATA
 GCAAAATGTAGGCTGCCTTTGTAAAAATTTGATGTGTTCCTGGCAGGATATCGAAAGAAC
 ATGTTTATTTTAAAAATTTATAACAAGTCATTTAAAGTCCAGTGTCTGAAAAATTTATATA
 AGTTTATACCTTTGATACGGAATTTACACAGGTAGGAGTGTATTAGTGGCAATGTGTAGG
 TTATGGATGGAGTGTGCTGCTATAAATGTAATGAATGAATTAATATCTACTTGGGTAGTA
 TGGCCTTTGCCAACAAAGTGAAGTGTTTTGGTTGTTTAACTCATGAAGTATGGGTTCAAGT
 GGAATGTTTGGGAAGTCTGAAGGATTTAGACAAAGGTTTGAAGAGGATAATCATGGGTTAGA
 AGGAAGTGTTTGAAAGTCACTTGAAGTGTAGTTTGGGCCAGCAGCGGTAGCTACCCCTT
 GGTAAATCCAGCATGTTGGGAGCTTAAGTGGGTAGTATCTTAGGCCAGGAATTCAGACACA
 GCTTGGGCACATGTTGAACTGTCTTATAAAAAATATCTGGCTTTGAGCATATGCTGTGGTC
 CAGCATCGAGAGGCTAGTGAAGATTGCTGAGCCAGAGCGCAAAGTGTGCAGTGGCAAGTCA
 CGTCACTGCACTCTAGCTGGCAGAGATGAGCCAAAAAATATATATATTTGAAATCAAGG
 AGGCAAAATTTGACAGGGAAGGAAGTAATGCAAAACCACTAGGCTTTAGTAGGTACTTAT
 ATAAATCTAGTCCAGTCTCTCATTTTAAAAAATGAAGACAGTGAATACAGACTAATAATA
 GCTCAGATAGCTAATTAGGAATTTCAAGTTGGCAATATAGCATTCTCTGTGACATTTAA
 AATAATTTCTATTTCAAATACATGCATATGTAATTTACACTCATACTGTGATAATTAATGT
 GATGTGGATTGCTGGTGTCCAGCATGACCCATAAACAGGTGAGAAGATGATGGAATGTTT
 AGAATAAATCTGCTGTATAGTATATACACAGTGTCAAAAGGTGTTAAATGCTTTTGAT
 TTACTGCCATGTAATGAAATATATAGATTTGTGAACCTTCAACCTGAAAAATCAAGCAGT
 ATGACAGTTTAGTATTTGTATGTGCATAGTGTCTAATGAAGCTTTAAATATCTCAACT
 TCTCTTTAAAAATTTTATTTAATGTGAATGGAATATAACAATTCAGCTTAATTCCCAACC
 TTATCTGTGTGATAGCATGTATTTGCCAACAATTTTGAATGGCTGTGTTTACCTCTAAATAA
 TTGAATTCAGAGAAAAAATAAAAAA

MGSVLGLCSMASWIPCLCGSAPCLLCRCPCSGNNSTVTRLIYALFLLVGVCVACVMLIPGME
EQLNKIPGFCENEKGVPNCNILVGKAVYRLCFGLAMFYLLSLLMIKVKSSSDPRAAVHNG
FWFFKFAAAIAIIIGAFFIPEGTFFTTVWFYVGMAGAFCFILIQVLVLLIDFAHSWNESWVEKM
EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYTHPASCSENKAFISVNMLLCVGASVMSI
LPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPETNCNPSSLIIIGYNTTSTVPKEGQSV
QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVKNLTLTDESTLIEDGGARS DGSLEDGDDVH
RAVDNERDGVTYSYFFHMLFLASLYIMMTLTNWSRYEPSREMKSQWTA VVVKISSWIGI
VLYVWTLVAPLVLTNRDFD

FIGURE 42

CGGAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCCGCTGCTTCTTGNGACGTTGTGGAGAT
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC
CCGTGTTTGCTATGCCGATGCTGTCTAGTGGAAACAANTCCACTGTAAC TAGATTGATCTA
TGCACTTTTCTTGCTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAG
AACAACTGAATAAGATTCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATT
TTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCT
CTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGAT
TTTGGTTCTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

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FIGURE 43

GTTATTGTGAACTTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC
CANGTTTGTGTGGAAGTGCCCCGTGTTTGNATGCCGATGCTGTCTAGTGGAACAANTCC
ACTGTAATTAGATTGATNTATGCACTTTTNTTGCTTGTGGAGTANGTGTAGCTTGTGTAAT
GTTGATACCAGGAATGGAAGAACAACCTGAATAAGATTCCTGGATTTTGTGAGAATGAGAAAG
GTGTTGTCCCTTGTAACATTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG
GCTANGTTCTATNTTCTTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCAGTGCACAATGGATTTTGGTTTTTTAAATTTGCTGCAGCAATTGCAATTATTATTG
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FIGURE 44

AAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC
GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATAACCATGTTTGTGTGGAAGTGCCCCGTGTT
TGCTATGCCGATGCTGTCTAGTGGAAACAACCTCCACTGTAAC TAGATTGATCTATGCACTT
TTCTTGCTTGTTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAAC
GAATAAGATTCCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATTTTGTTG
GCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTTTA
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGTT
CTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

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GCTGTCCTTAGTGGAACAANTCCAACCTGTAACCTGGATTGATCATGCACCTTTTCCTTG
CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGTTCCAGGATTGGANGAACAACTGAATA
AGATTCTCGGATTTTTGTGAGAATGAGAAAGGTGTTGCCCCCTGTAACATTTTTGGTTGGC
TATAAAGCTGTATATCGTTTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTCTTTACT
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCT
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCCAGAAGGAACTTT
ACAACTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTCATCCTCATACAACTAGT
CTTACTTATTGATTTTGACATTTCATGGAATGAATCGTGGGTGAAAAATGGAAGAAGGGA
ACTCGAGATGTTGGTATGCAGCCTTGTTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTA
GTTGCTATCGTCCTGTTCTTTGTCTACTACACTCATCCAGCCAGTTGTTCAGAAAACAAGGC
GTTTCATCAGTGTCAACATGCTCCTCTGCGTTGGTGCTTCTGTAATG

CTCGGGCGCGCACAGGCAGCTCGGTTTGCCCTGCGATTGAGCTGCGGGTCGCGGCGGGCGCCGGCCCTCTCAAATGCGAAATGTGTGTGCTGCTGGAGCGAGCGAGCGAGGCTTCGGCAAGAGCAGTGCAGTGTTCGACAGCCGGGCGAGTCTCTGTGAAGACGATAAAAGAAACATTTAATAGCTGATTACGAGAGGCGCCGGCGGGGCTGTGCGACTCCCGCGGAACTTTGGCTCCTCAGCTCCGAGGACGAGAGAAAGACGGAAGAAGGACGAGATTACCTGTGTTTCAGACCAAGTCAGCTGATGATGATGGCCCTCTGAATTTACAGATATTTGATTTAGGATGCGCCCTGTGTTGTGTGTACGCACACACAGTGCACACAGGCTCTGGCTCGCTCCCTCTGTTTCCAGCTTCCGGGCAATCCCATCTGTGTTTCAACTCTCCGCGAGGGCGAGGAGCGAGAGTGTGCAATCTGCGAGTGAAGAGGACGAGGGAAGAAACAAAGCCACGACGCACTTGAGACTCCGCGATCCCCAAAGAAGCACCGAGTACGACAAAAAAGAACTGGGCGCCCGGAGCTGTGCTGTGCTGTGCTGCTCCGCAACTGTGTTCTCCCTGTGGTGAGACTCGGCTCTCTGTGTCACACACCGCTTGAAGAGCGAGTTTCAGAGGACCCGAGAGACTTCCGCCCCACATCATCTGCTGTGACGCGACGACGAGTGTGAGAGCTGGGTTCCATGCAGGTGATGAACAAAGACCGCGGCTATCATGGAGCAGGGCGGGCGCACTTCAACCGCTTCTGACACCACTGTGTGCTGCCCTCAGCTGCTCTCATCTCTCATGCGAAGTACGCTCCAAACCAACCAAGCCTACACCAACATGAGAAGTGTCTCTCGCCCTCTGGCAGGCACGACAGAGCGACGACCTTTCGCTGTACTCAATGACCTGGCTACGGGACGCTTCTTCGGGAAGTATTCTAATGATCAACGGCTCTACTGCTGCCACCGGCTGGAAGAGTGGTGCGAGCTCTTAAAACTCCCGCTTTTATAACTACAGCTGTGTCGGAACGGGCTGGAAGACGAGACCGGCTCCGCACTCTCAAGGATTACCTTACAGACCTCATCAACATGACAGCTGAGCTTCTTCCGACGCTTCAAAGAGATGTACCCGACAGGCGGACTCTCTATGGTCATCAGCCATGCAGCCCCCAGCGGCTGAGGATTGAGGACCCCAACATTAACGCTCTTCCCAAGCTATCTAGCACTATCAGCATGAGCTACACTACGCGCTACCGCCCAACCGGACAAACATGGATCATGCGCTACACGGGCGCATGAGGCCATCGCCGATGGAATTCACCAACATGCTCAGCGGAAGCGCTTGCAGACCTCTATGTCGTGAGCAGCTCATGGAGACGATTACAACATGCTGGTTGAGACGGGCGAGCTGGACACACATGATCATGTATAACCGCGACACCGTTTACCACATCGGCCGTTTGGCTGCTGTAAGAGGAATCCGATTCGATATGAGTTGACATCAGGTCGCCGTTCTAGCTGAGGGGCCCCAAGCTGTGAAGAGCGGCTGCTGAATCCCGACATGCTCTCAACATTAAGCTTGCCCCACCATTCTGGACTTCAGGCTTCAGGCTGCACATACCTGCGGATATGACCGGGAATCCATCTCAAGCTGCTGGACCGGAGCGCGCGTGAATCGGTTTCACTTGAAAAAGAGATGAGGCTCTGGCGGGAATCTCTTGTGGTAGAGGAGCAAGCTGTCAACAAGAGACAAATGACAAGGTGAGCGCCAGGAGGAGAATTTCTGCCAAGTAGCAGCTGTGAAGAACTGTGTACGCTGCTGATACACAGCGGCTGTGACGCTGGGACAGAAAGTGGCAGTGTGTGGAGACCGCCAGGGAAGCTGAAAGCTGCAATAGTGAAGGCGCCATCGGCTGGGCGGAGCAGACGCCCTTCCAAACTCTGTGCCAAGTATACGGGTATACGGCGAGGCGAGGCGCTGACCTGTGACGCGGGGACTACAAGCTAGCCTGCGCGGACCGGGAAGAACTCTCAAAGAAGTACAAGGCAAGCTATGTCGCGAGCTGCTCATCGCTCATGTCAGCTCGAGTGGACGGAGGTTGACACGCTGAGGCTGGGTGATGCCCGGAGCCCCGAACCTCAACGCGGCACTGGCCAGSGGGCCCTGAGGACCAAGATGACAAGATGCTGGGACTTTCAGTGGCACTGGAGGCTCTCCGACTACTCAGCGCGCAACCCCTTAAGGTGACACATCGGTGCTACATCTAGAGAACGACACAGTCCA GTGTGACCTGGACCTGTACAAGTCCCTCGAGCGCTGGAAGACCAAGCTGCACATCGACACGAGATTGAACCCCTGCAAAATCAAGATTAAAGACTCTGAGGAGAACTCGAGGTAACCTGAGAAGAAAGCGGCCAGAGAAGATTGACGTGTCACAAATCAGATTACCAACACCCGACAGAGGCGGCTCAAGCACAGGCTCAGTGTGCATCTTTCGAGGAAGGCTCAGAGAAAGGACAAGTGTGGCTGTTCGGGAGCAGGAGCGCAAGAGAAGAACTCCGCAAGCTGCTCAGCGGCTCTGCAAGAACACGACAGCTGCAGCATGCGAGGCTCAGTGTCTTACCACGACACACAGCACTGGCAGACGCGGCTTTGCAACATGGGGGCTTTCTGTGCTTGCACCAAGCGCCAAACATACACGTACTAGTGTGTCAGGAGCACTCAATGAGACTACAAATTTCTCTGTGAATTTGCAACTGGCTCTTAGAGTACTTTGATCTCACACAGACCCCTACAGCTGTGAATGCAGTGAACCATGACAGGAGTGTCTCAACAGCTACAGCTACAGCTCATGAGCTGAGGAGCTGCAAGGGTTACAAGAGTGTAAACCCGGAATCGAAACATGGAATGGAATGGAGGAGTGTGACATGACATAACAGGACTTTCCAGCTACAGGACTTACAGGACTTTCTCAAAATCTGCTGGGACAACTGTGGGAAGGCTGGGAAGCTGGGAAGCTTAAAGAAACATGTGGTGATTTCCAGCAGACCTGTGCTATTGGCCAGAGAGGCTGAGAAGCAAGCAAGCACTCTGAGTCAACATGACATTTCTGGAGATAACCGAGGACGAGATAACTTCAGGAAGCTATTTTGGCCCTGCTTTTGGCTTTGATTTGTTTGGATTATATCTCACCAGTGCACCAATGCAAGATGAGATGAGATTTTCTGTAATATATCTCAAAAGAGCTTCAAAAGAGCACTCAAAAGAGCACTGAAGAACTGAAGAAAGCAAGGACAGGCAAGCTGGAGAGCTTGAACATTAACATCAACATGGAACCTTTAGGCGAACCTTAATAAGAAATCTGCCCTTATCTATATGTGACTATTTACATGTAATCAACATGGAACCTTTAGGCGAACCTTAATAAGAAATCCCAATTTTCAGAGTGGTGGTGTCAATAAAGCTCTGTGGCGAGTGAAGAAGAAAA

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRNRIRPNIIILVLTDDQDVELGSMQ
VMNKTRRIMEQGGAHFVTTMPCCPSRSSILTKGYVHNHNTYTNNENCSSPSWQAQHE
RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGS
YSKDYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRSLFPNASQHITP
SYNYAPNPDKHWIMRYTGPMPKPIHMEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNT
YIVYTADHGYHIGQFGLVKGKSMPEYFDIRVPFYVRGPVNEAGCLNPHIVLNIIDLAPTILDI
AGLDIPADMGKSIKLLDTERPVNRFLHKKKMRVWRDSFLVERGKLLHKRDNDKVDAAQEN
FLPKYQRVKDLCQRAEYQTACEQLGQKWQVEDATGKCLKHKCKGPMRLGGSRALSNLVPKY
YGGGSEACTCDSGDYKLSLAGRRKKLFKKKYKASYVRSRSIRSVAIEVDGRVYHVGLGDAAQ
PRNLTKRHWPGAPEDQDDKGGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDLDLYKS
LQAWKDHKLHIDHEIETLQNKIKNLREVRGHLKKRPEECDCHKISYHTQHKGRCLKHRGSSL
HPFRKGLQEKDKVLLREQKRKKLRKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLG
PFCACTSANNNTYWCMTINETHNLFCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL
HVQLMELRSCKGYKQCNPRTNMDLDGGSYEYQYRQRRKWPEMKRPSSKSLGQLWEGWEG

FIGURE 48

AACAAAGTTCAGTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA
GCTGCTGGGCAGAGAGGGACTGTCCGGCTCCAGATGCTGGGCCTCCTGGGGAGCACAGCCC
TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCTGCTGCTGCTGCTGCTGGCCACC
TGCCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGAA
CCGAGTCCGCGGGGGCCAGCCTTGCGCCCTTCCGGCGGCGGGGCCACCTGGGAATCTTTCACC
ATCACCGTCATCCTGGCCACGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACCAC
CCCCGCCACACCCCTCACCACCTCCACCACCACCACCACCCCCACCGCCACCATCCCCGCCA
CGCTCGCTGAGGGCTGCTGTCGCCGGTGCCGTGGACAGCAGCTGCCCTGCCCTCCCATCTG
TTCCAGGACAAGTGACCCCATGTTCATGTGGAAGGATGCATCTCTGGGGTGAACGAGG
GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTTGCATGGCATGCCCCAGTGTAATATGGC
AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGCTGAAGGGTTTGGGGAGTGGAGAGCAAGG
GTGCTCTTTCGGGGCTGGACAGCCCGTCTTGTGACAGTGACTCCAGTGAGCCCCAGAAATG
ACAAGCGTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTC
ATCAGGCTGCTGCAGGCCTCTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAATGTCCTTTT
GGTTTGGAGAAGGCAGTGTGAGGCTGCACAGTCAATTTCATCGGTGCCTTAGTCCAAGAAAAT
AAAAACCACTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA

MLGLLGSTALVGWITGAAVAVLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRRRAQPPWFR
RRGHLGI FHHHRHPGHVSHVPNVGLHHHHHPRHTPHHLHHHHHPHRHHPRHAR

FIGURE 50

GGCGGCTGCTGAGCTGCCTTGAGGTGCAGTGTGGGGATCCAGAGCC**ATG**TCGGACCTGCTA
CTACTGGGCCTGATTGGGGGCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGG
GTACTCAGGGCTACTGGCTGGGGTGAAGTGAGTGCTGGGTACCCCCATCCGCAACGTCA
CTGTGGCCTACAAGTTCACATGGGGCTCTATGGTGAGACTGGCGGCTTTTCACTGAGAGC
TGCAGCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCACATGGTGCC
CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCC
CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC
CATGTGGTGACAGCCACCTTCCCTTACACCACCATTCTGTCCATCTGGCTGGCTACCCGCCG
TGTCCATCCTGCCTTGGACACCTACATCAAGGAGCGGAAGCTGTGTGCCATCCTCGGCTGG
AGATCTACCAGGAAGACCAGATCCATTTTCTGTGCCCACTGGCACGGCAGGGAGACTTCTAT
GTGCCTGAGATGAAGGAGACAGAGTGGAAATGGCGGGGGCTTGTGGAGGCCATTGACACCCA
GGTGGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGAAGTGAGCC
CTGGCAGCCGGGAGACTTCAGCTGCCACACTGTACCTGGGCGGAGCAGCCGTGGCTGGGAT
GACGGTGACACCCGAGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGA
GGAGCTGGACTTGGAGGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGACCCTGGGACTGAGC
CCCTGGGGACTACCAAGTGCTCTGGGAGCCCACTGCCCCTGAGAAGGGCAAGGAG**TAA**CCC
ATGGCCTGCACCCTCCTGCAGTGCAGTTGCTGAGGAACTGAGCAGACTCTCCAGCAGACTCT
CCAGCCCTCTTCTCCTTCTCTGAGGGAGGAGGGGTTCTGAGGGACCTGACTTCCCTGC
TCCAGGCCTCTTGCTAAGCCTTCTCCTCACTGCCCTTTAGGCTCCCAGGGCCAGAGGAGCCA
GGGACTATTTTCTGCACCAGCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTTTTCACTC
ACAGTGAGCTTCCAGGACCAGAATAAAGCCAATGATTTACTTGTTTACCTGGAAAAAAA
AAAAA

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGlyETGR
LFTESCSISPKLRSIAVYYDNPHMVPDPKRCRAVGSILSEGEESPSPELIDLYQKFGKVF
FPAPSHVVTATFPYTTILSIWLATRVRVHPALDITYIKERKLCAYPRLIYQEDQIHFMCLAR
QGDFYVPEMKETEWKRWGLVEAIDTQVDGTGADTMSDTSVSVLEVSPGSRETSAAATLSPGAS
SRGWDDGDTRSEHSYSESGASGSSFEELDLEGGPLGESRLDPGTEPLGTTKWLWEPTAPEK
GKE

FIGURE 52

CCGCGGGAACGCTGTCCTGGCTGCCGCCACCCGAACAGCCTGTCCTGGTGCCCCGGCTCCCT
GCCCCGCGCCAGT**CATG**ACCCTGCCCCCTCACTCCTCCCCTCCATCTGCTGCTGCTGCT
GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA
CCCTCCAAGTGGAGACCCCTGGTGGAGCCCCCAGAACCATGTGCCGAGCCCGTGCTTTTGGA
GACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT
GACCAGAGACCCTCTGGTTATAGAAGCTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGA
GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTGGCCTAT
GGAAAACGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT
GATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTCTTGCCTCTGGTAG
GGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAAT
AGACCCAAAGTCTCCAAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAA**TA**
ATAAATAATAAATTTTAAAAAAGCTAAAAAAGAAAAAAGAAAAA

MTLRPSLLPLHLLLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFGDTLHI
HYTGS�VDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLLDMCVGEKRRAIIPSHLAYGKRGF
PPSPADAVVQYDVELIALIRANYWLKLVKGIPLVGMAMVPALLGLIGYHLYRKANRPKVS
KKKLKEEKRNSKKK

FIGURE 54

CCCGGGAACGTGTTCTGGCTGCCGCACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCTGC
CCCCGCGCCAGTCATGACCCTGCGCCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGC
TGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACC
CTCCAAGTGGAGACCCTGGTGGAGCCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGAGA
CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA
CCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTCTCACTTGGCCTATGG
AAAACGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA
TTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTTGCCTCTGGTAGGG
ATGGCCATGGTGCCACCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAATAGA
CCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATAATA
AATAATAAATTTTAAAAAACTTA

CCGAAAGTCCCGTCCGGACCTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCC
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACCGGAAGCTTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGGAACGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGT
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGG
GCATTTTGCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC
CTATACAGAAAGGCCAATAGACCCAAAGTCTCAAAAAGAAGCTCAAGGAAGAGAAACGAAA
CAAGAGCAAAAAAGAAATAATAAATAATAAATTTTAAAAAACTTAAAA

FIGURE 56

CTGCTGCATCCGGGTGTCTGGAGGCTGTGGCCGTTTTGTTTTCTTGGCTAAAATCGGGGGAG
TGAGGCGGGCCGGCGCGGCGACACCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTG
ACCTGAAAAAAATGCTCTGGATTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGG
GAAAAGCGCAATACTATTGCTTCCATGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGAT
TATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCT
GTGGTGTTATAGCAACCATAGCCTTCCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGA
GGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGG
TTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTG
CTAAAGAAAAAGACATAGTATACCCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATCTTT
TTTGGAGGGCTGGTTTTTAAAGTTTGCCGCACTGAAGACTTATGGCAGTGAACACATCTGAT
TTCCACAGCACAAACAGCCCTGCATGGGTTTGTGTTTTTTTACTGCTCACTCCCAACCTT
TTGTAATGCCATTTTCTAAACTTATTTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACT
AAAATCACGAGAACACCTAAACAACAACCAAAAATCTATTGTGGTATGCACTTGATTAACCT
ATAAAATGTTAGAGGAACTTTCACATGAATAATTTTTGTCAAATTTATCATGGTATAATT
TGTA AAAAATAAAAAGAAATTACAAAAGAAATTATGGATTGTCAATGTAAGTATTTGTCATA
TCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTTAATGTGTTTATTCAAATGTGGT
CTCTTCTGTGTCAAATGTTAAATGAAATATAAACATTTTTTAGTTTTTAAAATATTCCGTGG
TCAAAATTCTTCTCACTATAATTGGTATTTACTTTTACCAAAAATTCTGTGAACATGTAAT
GTA ACTGGCTTTTGAGGGTCTCCCAAGGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCAT
GGTCCAGCCACCAGGCTCCCTGTGTCCCTTCCATGGGAAGGTCTTCCGCTGTGCCTCTCATT
CCAAGGGCAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCACTC
CACATCCACCACTG

MSGFLEGLRCSECIDWGEKRTIASIAAGVLFFTGWWIIIDA AVIYPTMKDFNHSYHACGVI
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWL FVGFM LAFGSLIASMWILFGGYVAKEK
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

TTCTTGGCTAAAATCGGGGGAGTGAGGCGGGCCGGCGCGGCACACCGGGCTCCGGAAC
ACTGCACGACGGGGCTGGACTGACCTGAAAAAATGTCTGGATTCTAGAGGGCTTGAGATG
CTCAGAATGCATTGACTGGGGGGAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGATC
TATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTATTATCCCACCATGAAAGAT
TTCAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGCCTTCCTAATGATTAATGC
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTG
CTCGCATTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGG
ATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCCGGAATTGCTGTATT
TTTCCAGAATGCCTTCATCTTTTTTGGAGGGCTGGTTTTTAAGTTGGC

FIGURE 59

TGGACGGACCTGAAAAAATGTTTGGATTNTAGAGGGNTTGAGATGTTCAGAATGCATGAC
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGTANTATTTTTTACAGGCTG
GTGGATTATCATAGATGCAGNTGTTATTTATCCCACCATGAAAGATTTCAACCANTCATACC
ATGCCTGTGGTGTTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA
GTCCGAGGTGATAGTTACAGTGAAGGTTGTTTGGGTCAAACAGGTGCTCGCATTTGGCTTTT
CGTTGGTTTCATGTTGGCCTTGGATCTCTGATTGCATCTATGTGGATTCTTTTGGAGGTT
ATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGNTGTATTTTTCCAGAATGCCTTC
ATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGANTTATGGCAGTG

FIGURE 60

GGACACCGGGTTCCGGACCAATGCANGACGGGGTGGANTGACCTGAAAAAATGTTTGGATT
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT
CCATTGCTGCTGGTGTACTATTTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT
TATCCCACCATGAAAGATTTNAACCACTCATACCATGCCGTGGTGTATAGCAACCATAGC
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT
GTTTGGGTCAAACAGGTGNTCGCATTTGGCTTTTCGTGGTTTCATGTTGGCCTTTGGATTT
CTGATTGNATTCTATGCGGATTCTTCTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTAT
ACCCTGGAATTNCTNTATTTTTTCCAGAATGCC

FIGURE 61

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGTGTANTATTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT
ATCCCACCATGAAAGATTTNAACCANTCATACCATGCCTGTGGTGTATAGCAACCATAGCC
TTCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTTGGGTCAAACAGGTGNTNGCATTTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN
TGATTGCATTTATGTGGATTNTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

FIGURE 62

GGGAGGCTGTGNCCGTTTTGTTTTNTTGGCTAAAATCGGGGGAGTGAGGCGGGCCGGCGCGG
CGNGACACCGGGTTCCGGGAACCATTGCACGACGGGGTGGACTGACCTGAAAAAAATGTTTG
GATTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATT
GCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT
TATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCA
TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA
GGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGG
ATNTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAG
TATACCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATNTTTTTTGGAGGGCTG

CCGACGCCGGCGTGA**ATGT**GGCTTCGGCTGGTGCTGCTCCTGGCTGTGCTGCTGCTGCTGCCGCTCTCTGCAAGTTTACTTTGGGCACTATTCTCTGGCAGCTCCCCAAGCTTTCTCTCGAAGATGTCTAAACGCCGCCACGCCCTGGTATGACAGCAAGGAGGCCAGGAAGACCTTTCTCAAAACAAGCTTTTTTCAGCCAAACCAAGTCCGGGAGAGCTGGATGTGGTGTTGAATTTGGCATGGCTTTTGGGGCGCTGGCTGCAGCTGCAATTCTAGCTAAAGCTGGCAAGCGAGTCTCTGGTCTGGGAACAACTACCAAGCGAGGGGGCTGTCTCATACCTTTGGAAGAAATGGCCTTGAAATTTGACACAGGAATCCATTACATTTGGCGTATGAAGAGGCGACATTTGGCCCTTTTATCTTGGACAGATCACTGAAGGCGAGCTGGACTGGGCTCCCCGTGCTCCTCTCCTTTTGACACATGTGTACTGTGAAGGGCCCAATGGCCCAAAAGGATACCCCATATTCCTGGAGAGAGACCTACATTCAGGCGCTCAAGGGAAGTTTCCACAGGAGGAAGCTATCATTTGACAAGTATATAAGCTGGTTAAGGTGGTATCCAGTGGAGGCCCTCATGCCATCTCTGTGAAATTCCTCCATTTGCCGTGGTTTCAGCTCTCTCGACAGGTTGGGCTGCTGACTGTTTTCTCTCATTTCTCAAGCATACCACAGAGCTGGCTGAGGTCTCGACAGCTGGGGGCTCTCTGAGCTCCAGGCAGTACTCAGTACATCTATCTCCCCATCTAGGTTGTCACCCCAACACAGTGCCTTTTTCATGCACGCCCTGCTGGTCAACCACTATGTAAGAGGCTTTTATCCCGAGGGGTTCAGTGAATTTGCCTTCCACACCATCTCCCTGTGATACCGGGTTGGGGCGCTGTCTCACAAAGGCCACTGTGCAGATGTGTTGCTGGACTCAGCTGGGAAAGCCTGTGGTGTCAGTGTGAAGAGGGGCATGAGCTGGTGAACATCTATTGGCCCATGCTGGTCTCAACGCGAGGCTGTTTCAACACTATGAACACTCTGCGGGGGAACGCGCTGCTGCTGCCAGGTGTGAAGCAGCAACTGGGGACGCTGCGGCCGCTTAGGCATGACCTCTGTTTTCATCTGCTCGCAGGACAGCCACAGGAAGACCTGCATCTGCCCTCCACCACTACTATGTTTACTATGACACGGCATTTGACCAGGGCGATGAGCGCTACGTCTCCATGCCCGAGGAAGGCTCGGAAACACATCCCTCTCTCTCTGCTTTCCCATCAGCCAAAGATCGCACCTGGGAGGACCATTTCCAGCGCGCTGAGGACCATTTCCAGCGCGCTGCACCATGATCATGCTCATACCCACTGCTACGAGTGGTTGAGGAGTGGCAGGCGGAGCTGAAGGGAAGAGCGGGGCAGTGCACATAGACACTTTCAAAACTTTTTGTGGAAGCCTCTATGTTCAGTGGTCTTGAAACTTTCCACAGCTGGAGGGGAAGGTGAGAGTGTGATCGAGATCCCCATCCCCACTCACCAACCACTTCTATCTGCGCTCTCCCCAGGTTGCCGTCTACGGGGTGCACCATGACTGGCGCGCTGCACCTTTGTGTGATGTCGCTCTTGGAGGCCAGAGCCCCATCCCCAACCCTCTATCTGACAGGCGAGGATATCTCACTGTGAGCTGTGCGGGCCCTGCAAGGTCCCTGCTGTGCAGACGGCCATCTGAAGCGGAACCTTTGACTACGACCTTAAGAATCTTGATTCTAGGATCCGGGCACAGAAAGAAAT**TAGT**TTCCATCAGGGGAGAGTCACAGGAAATTTGCCCAATGGCTGGGGCATCTCCCTTGACTTACCATAATGTCTTTCTGCATTAGTTCCTTGCAGCTATAAAGCACTTAATTTGGTCTGATGCCGTGAAGAGAGGCTGAGTTTAAATACAAATCCGAATCTGGGGCAATCGGGAATCAGCTGCTTCCAGCTGGGCGAGGTGAGTCTTTAGCCTTTTATAACATGCCATCCCTACTAATAGATATATGACTTGGATAGCTTGATGTCTCATGACAGCGCGCTCTGCATCTCCCTCACCCATCCCTACTCATGATCAATCAAGGCAATATTCCATCTGTGATAGAACCCTGGCAGTTGTTCAGCTCAACCTGGTGGGTTTCAGTCTGTGCTGAGGCTCTGCTCTCATTCATTATTAGTGCTACGCTGCACAGTTCTACACTGTCAAGGAAAAGGAGACTAATGAGGCTTAACTCAAAACCCTGGCGGTGGTTTGGTTGCCATTGCATAGGTTTGGAGAGCTATAGATCTCTTTTGTGCTGGGTTGAGTGGCTCTCCAGGGAGACGAAATGCTGTGCTGTGCGCAGTGTGTTCTGGAGCTTTGGGTTACAGCAGGATCCATAGCTTAGTATGGTGCTATGCAGATCATATCCAATCATATGGAAGTCCCGGCTGCTCTTCCCTTATCATCGGGGTGGCAGCTGGTTCTCAATGTGCCAGCAGGACCTAGTACTGAGCTTACGCTCAATCAAGCTTATCCACCAATACACAGGAAGGTTGATGCAGGGAAGGTTGACATCAGGATTCAGGCAATGAGCATTGGTATAGATATCTTTGCTGGGCTGAAGCAGGCTGACGAGGGAAGGTTGAGGGAAGGGAAGCCAGAGGGAAGGGAAGCCAGGAGGTGTGGGTAAGGGAGGGAAGTGCATCAGAAAAGGGAAGCCAGGAATGTGTGTGAAGCCAGAAATGTCATTTGAGTTAATAGCACATGTGAGGTTAGACAGGTTAGTGTGAATGCACCTCAAGTTTGGTAAATGACTTTTTCAGTTATGTCTTTGTATCAGACATACGAAGGCTCTTTTGTAGTGTGTTAATGTACATTAATAAATTTATGTATTCCTTTCGTTTTAAAAAATAAAAAA

MWLPLVLLLA VLLLA V LCKVYLGLFSGSSPNPFSE DVKRPAPLVT DKEARKVKLQAFSAN
 QVPEKLDVVVIGSGFGLAAAA I LAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIG
 RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNGRKEYPMYSGEKAYIQGLKEKFPQ
 EEAIIDKYIKLVKVVS GAPHA ILLKFLPLPVVQLDRCGLLTRFSPFLQASTQSLAEVLQQ
 LGASSELQAVLSYIFPTYGVT PNHSAFSMHALLVNHYMKGGFYPRGGSSEIAFHTIPV IQRA
 GGAVLT KATVQSVLLDSAGKACGVSVKKGHEL VNIYCPVVSNAGLFNTYEHLLPGNARCLP
 GVKQQLGTVRPLGMTSVFICLRGTKEDLHLPSTNYVYYDYDTMDQAMERYVSMSPREEAAEH
 IPLLFFAFPSAKDPTWEDRFPGRSTMIMLIPTAYEWFEEWQAE LKGKRGSDYETFKNSFVEA
 SMSVVLKLFPPQLEGKVESVTAGSPLTNQFYLAAPRGACYGADHDLGR LHPCVMASLRAQSPI
 PNLYLTGODIFTCGLVGALQGALLCSSAILKRNLYSDLKNLDSRIRAQKKKN

FIGURE 65

[illegible]

MRVRIGLTLLLCVALLSLASASSDEEGSQDESLSKTTLTSDSESVKDHTTAGRVVAGQIFLD
SESELESSIQEEDSLKSQEGESVTEDISFLESPNPENKDYEEPKKVRKPALTAIEGTAHG
EPCHFFFLFDKEYDECTSDGREDDRLWCATTYDYKADEKWGFCETEEEAARRQMQEAEEM
YQTGMKILNGSNKKSQKREAYRYLQKAASMNHTKALERSVYALLFGDYLQNIQAAREMFEK
LTEEGSPKQGATLGLYASGLGVNSSQAKALVYYTFGALGNNLIAHMLVLSRL

CTTCCCAGCCCTGTGCCCAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT
GCCTCCCTGCCTCTGGCCATGGCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGACCTTCCT
GTCAGTTTCCAGACAGTCTGGCCAGCTGGATGCACTGCTGGTCTTCCAGGCCAAGTGG
CTCAACTCTCCTGCACGCTCAGCCCCAGCACGTACCATCAGGGACTACGGTGTGTCTTG
TACCAGCAGCGGGCAGGCAGTGCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA
CCACCGGCCTGTGTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCACAATGCCT
GTGTCTCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC
TACGGCTTTAGTCCCTAGGGGTGGGGTGTGAGATGGGTGCCTCCCCCTCTGCCTCCCATTCT
GCCCCTGACCTTGGGTCCCTTTAAACTTTCTCTGAGCCTTGCTTCCCCCTCTGTAAAATGGG
TTAATAATATTCAACATGTCAACAAC

MACRCLSFLMGTFLSVSQTVLAQLDALLVFPQGVAQLSCTLSPQHVTIRDYGVSWYQQRAG
SAPRYLLYRSEEDHHRPADI PDRFSAAKDEAHNACVLTISPVPEDDADYYCSVGYGFSF

FIGURE 69

GCGCGCCCGCCCCGAGACCGGGCCCCGGGGCGCGGGGCGGGGATGCGGGCGCCGGGGCGG
 CGATGACCGCGGAGGCGACGCGCGGGCCCCGGCCCTGACCCCGCGCGCCCGCGCTGAGCCCC
 CCGCGCGAGGTCCGGACAGGCGCGAG**ATG**ACGCGCGAGCCCCCTGTGTGCTCTGCTGCTGCCGCG
 CGCTGCTGCTGGGGGCGCTTCCACACGGCGCGCGCGCGCGGAGCGCCCCAAAGATGCGGGGAC
 AAGGTGGTCCCACGCGAGGTGGCCCGCTGGCGCGCACTGTGCGGCTGCAGTGGCTCCCAATGGA
 GGGGGACCCGCGCGCTGACCATGTGGACCAAGGATGGCCCGCACCATTCCACAGCGGCTGGA
 GCCGCTTCCGCGTGTGCGCGAGGGGCTGAAGGTGAAGCAGGTGGAGCGGGAGGATGCCGCG
 GTGTACGTGTGCAAGGCCACCAACGGCTTCCGCGAGCTGAGCGTCACTACACCCCTGCTCGT
 GCTGGATGACATTAGCCCAGGGAAGGAGAGCTGGGGCCCGACAGCTCCTCTGGGGGTCAAG
 AGGACCCCGCCAGCCAGCAGTGGGACGACGCGCTTCAACAGCGCTTCCAAGATGAGGCGC
 CGGTGTATCGCACGGCGCGTGGGTAGCTCCGTGCGGCTCAAGTGCCTGGCCAGCGGGACCC
 TCGGCGCCGACATCACGTGGATGAAGGACGACAGGCGCTTACGCGCGCCAGAGGCGCGCTGAGC
 CCAGGAAGAAGAAGTGGACACTGAGCTGAAGAACCTGCGCGCGGAGGACAGCGGCAAAATAC
 ACCTGCCGCGTGTCAAGCCGCGCGCGCGCCATCAACGCCACCTACAAGTGATGTGATCCA
 CGGAGCCCGTCCAGCCCGTGTCTACAGGACGCGACCCCGTGAACACGACGGTGGACTTCG
 GGGGGACACGTCCTTCCAGTGAAGGTGCGCAGCGACGTGAAGCCGGTGTATCCAGTGGCTG
 AAGCGCGTGGAGTACGGCGCCGAGGGCGGCCACAACTCCACCATCGATGTGGGCGGCCAGAA
 GTTTTGGTGTGCTGCCACGGGTGACGTGTGGTTCGCGGCGCGAGCGGCTCCTACCTCAATAAGC
 TGTCTACCTACCGTGGCGCCGAGGACGATCGGGCATGTACATCTGCGCTTGGCGCCAAACCC
 ATGGGCTACAGCTTCCGACGGCGCTTCTCACCGTGTGCGAGACCCAAACCGCCAGGGCC
 ACCTGTGGCGTCTCTGCTCTCGGCCACTAGCTGCGGTGGCCGCTGTCTCGGCATCCAG
 CCGGCGCTGTCTTACTCTGGGCACCTGCTCTGTGGCTTTGCCAGGCGCCAGAAGAAGCCG
 TGCACCCCGCGCGCTGCCCTTCCCTTGGCTGGGACCGCGCCCGCGCGCGCGCGCGCGCG
 CAGCGGAGACAAGGACCTTCCCTCGTTGGCGCGCTTACGCGCTGGCCCTGGTGTGGGGTGT
 GTGAGGAGCATGGGTCTCCGGCAGCCCCCAGCAGCTTACTGGGCGCCAGGCGCCAGTTGCTGGC
 CCTAAGTTGTACCCCAAATCTACACAGACATCCACACACACACACACACATCTCACAC
 ACATCACACGTTGGAGGCAAGGTCCACCAGCACATCCACTATCAGTGC**TAG**ACGGCACCGT
 ATCTGCAGTGGGCGCGGGGGCGCGGCGAGACGACGATGGGAGGATGGAGGACGGAGCT
 GCAGACGAAGGCAGGGGACCATGGCGAGGAGGAATGCGCAGCACCCAGGCGAGTCTGTGTG
 TGAGGCATAGCCCTGGACACACACACACACACACACTACCTGGATGCATGTATGCAC
 ACACATGCGCGCACACGCTGCTCCCTGAAGGCACACGTACGCACACGCACATGCACAGATG
 CCGCCTGGGCACACAGATAAGCTGCCCAAATGACGCGACACGCGACAGACATGCCGAACA
 TACAAGGACATGCTGCTGAACATACACACGACACCCATCGCAGATGTGCTGCCTGGACA
 CACACACACACACGGATATGCTGTCTGGACGACACACGTCAGATATGGTATCCGGACACA
 CACGTGCACAGATATGCTGCTGGACACACAGATAATGCTGCCTTGACACACACATCCAGG
 ATATTGCTGGACACACACACACACACGCTGCACAGATATGCTGTCTGGACACGCACAC
 ACATGCAGATATGCTGCTGGACACACACTTCCAGACACACGTCACAGGCGCAGATATGCT
 GCCTGGACACACGCAGATATGCTGTCTAGTCACACACACGCGACAGATGCTGTCCGGACAC
 ACACACGCATGCACAGATATGCTGTCCGGACACACACGCGACGAGATGCTGCCTGGAC
 ACACACACAGATAATGCTGCCTCAACACTCACACACGTGCAGATATTGCTGGACACACACA
 TGTGACAGATATGCTGTCTGGACATGCACACACGTCAGATATGCTGTCCGGATACACACG
 CAGCGACACATGCAGATATGCTGTGCTGGGACACACTTCCGGACACATGCACACACAGGT
 GCAGATATGCTGCTGGACACACACACAGATAATGCTGCTTCAACACTCACACACGTCGAGA
 TATTGCTGGACACACACATGTGCACAGATATGCTGTGCTGGACATGCACACGTCGAGATA
 TGCTGTCCGGATACACACGCGACACACATGCAGATATGCTGCTGGGACACACTTCCGGA
 CACACATGCACACACAGGTGCAGATATGCTGCTGGACACACGAGCTGACGCTCTTTGG
 GAGGGTGTGCCGTGAAGCCTGCAGTACGTGTGCCGTGAGGCTCATAGTTGATGAGGAGCTT
 CCTGTCTCCACCGTCTACTCCCCCACTCTGCGCGCCTGTCTCCCGCCTCAGTCCCGCCT
 CATCCCGCCTCTGTCCCTGGCCTTGGCGGCTATTTTTGCCACCTGCTTGGGTGCCGAGG
 AGTCCCTACTGCTGTGGGCTGGGGTGGGGGACAGAGCCCAAGCCTGAGAGGCTGGAG
 CCGATGGCTAGTGGCTCATCCCAGTGCAATTTCCCTTGACACAGGAAGGGGCGCTGGTA
 TTTATATTTAAGAAATGAAGATAATATTAATAATGATGAAGGAGAGCTGGGTTCAGGAG
 TGTGGTCTCTCTGGGGCGCGGACCCGCTGGTCTTTGAGCCATGCTGATGACACACCC
 GTCCAGGCGACACACCCCGCCACCCACTGTGCTGGTGGCGCCAGATCTCTGTAAATTTTA
 TGTAGAGTTTGAAGTGAAGCCCGTATATTTAATTTATTTTGTAAACAAAA

MTTPSPLLLLLLPPLLLGAFPPAAAARGPPKMAADKVVPRQVARLGRTVRLQCFVEGDPPPLTM
WTKDGRTHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVLDDISPGK
ESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRRIARVPGSSVRLKCVASGHPRPDITWMK
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTSRKPV
TGTHPVNTTVDFGGTTSFQCKVRSVDPKPIQWLKRVEYGAEGHRNSTIDVGGQKFVVLPTGD
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVLPDPKPPGPPVASSSSA
TSLPWPVVGIPAGAVFILGTLTLLWLCQAQKKPCTPAPAPPLPGRHPPGTARDRSGDKDLP
LAALSAGPGVGLCEEHGS PAAPQHLLGPGPVAGPKLYPKLYTDIHTHTHTSHTHSHVEGKV
HOHIHYOC

FIGURE 71

CCCAGCTGAGGAGCCCTGCTCAAGACACGGTCACTGGATCTGAGAAACTCCCAGGGGACCGCATTCCAGAGTCT
 AGTGACTCTGTGAAGCACCCACATCTACCTCTTGCCACGCTTCCCACGGGCTGGGGGAAAGATGCTGGGGGACCA
 AGGCCTGGGTGTTCTCCTTCCCTGTGCTGGAAAGTACATCTGTGTTGGGGAGACAGACAGTCTCACCGCTCA
 GTAAGAGAGATCCAGCCTGGGGAAGAAAGAACCCAGCATCTTTGCCAAGCCTGCCGACACCCCTGGAGAGCCCTGG
 TGAGTGGACCAACATGGTTCAACATCGACTCCAGCGGGGAGGGCCACTATGAGCGGCTGGAGGCCATCTCCGT
 TCTACTATTGGGACCGGTGTATGTGCGCGCTCCCTGCGGCTAGAGCCTTCCGACACTCTACGACACTCGGACCTCGCGGC
 GCACTGGGCGAGGTGGTCCATGGTAGCTCCGCTGAGGCTTTCTGGTCCCTCCACAGGAGACAGCGCCCTGGGCCA
 GAACCTGCTCTAATTACACCGTACGCTCCCTGCGCCACAGGATCCCTCGCCCGAGACACAGAGCGCATCTGGGA
 GCCATGTGCTCCTCGAGAGATGCTCAGCTGCTGTGGTACAGCTGGGGTCCAGACTCGCACACGCATTTGGC
 TTGGCAGAGATGGTGTGCTGTGCTGACAGGCGAGGAGGGGTGAGCTGATGGCGAGGACTGTACAGC
 CTGTGACCTGACCTGCCAATGGGCCAGGTGAATGCTGACTGTGATGCCGTGCATGGCGAGGACTCATGTGCTTC
 ATGGGGCTGTCTCCTTCCCGGAGGTGCCACGCCCTAGGGGCTGCTATCTACTCCTGACCAAGACGCCGAAG
 CTGCTGACCCAGACAGACAGTGTAGGGAGATTCCGAATCCCTGGCTGTGCGCTGATGGCAGAAAGCATCTGAA
 GATCACAAAGGTCAGATTGTCGCCCATTTGACTACAAATGCCAAGACTAGCCTGAAGGCAGCCACCATCAAGG
 CAGAGTTTGTGAGGGCGAGAGACTCCATACATGGTGATGAACCTTGAGACAAAAGCAGGAGAGCTGGGCAGAGC
 GTCTCTGTGCTGAAGGCCACAGGGAGGCCAGGCCAGACAAGTATTTTGGTATCATATGACATTTGCT
 GGATCCTTCCCTCTACAAAGCATGAGAGCAAGCTGGTGCTGAGGAAACTGCAGCAGCAGCAGGCTGGGGAGTACT
 TTTGCAAGGCCAGAGTGTGCTGGGGCTGTGAAGTCCAAGGTTGCCAGCTGATGTGCACAGCATCTGATAG
 ACTCCTTGGCAACCCAGTCTCCTGAGAGCTATCTTATCCGGCTGCCCATGATTCTCTTCAAGATTCCACCACTC
 CTCTTACTATGAGCTGGGAGGCTGCCCTGTTAAAGACTGTGCGAGGCGAGCAGAGTAAATGGGATCAGGCTG
 ATGCTGTGAGAACTGTGTGGCATCTCCAAGCAGAGGAAAGGGAGTCCAGTGGAGGAGTGGCTACAGCTACCC
 ACCAAGTGGCCAAAGAGTGCACCTGGCCAGCGGTCTACGAAATCCGAGACTCGTGGGGGCGCTGTGACGTGC
 TGCTGACATGAGAGCCCATGGCTTTGGCATGTGTACATGGGGAACGCCGTGTAAAGCATGACTGGCTACCA
 AGGCACTTCTACCTCCATGTGCCCGAGACACTGACAGGCTGGTGTCTACATTTTGGGACAGGCTGCAAGAG
 TTTGTCAACACCAAGATGCTACTCTTTCAACAAGAGGGGAGTGCCGTGTTCCATGAATCAAGTATGCTTCG
 TCGGAAGAGCCCATCACTTTGGAAGCATGGAGACCAACATCATCCCCCTGGGGGAGATGGTGTGGTGAAGACC
 COATGTGCTGAATCTAGACTTCCATCCAGGAGTTCTACAGGCAGAAATGGGGAGCCATAGTGAAGAAAGTGAAG
 GCGAGTGTGACCTTCTGGATCCCGGGAATTTTCCACAGCCACAGCTGCCAGACTGACCTGAATCTCATCAA
 TGACGAAGGAGACACTTTCCCTTTCGGACGTATGGCATGTTCTCTGTGGACTTCAGAGATGAGGTCACTCAG
 AGCCACTTAATGCTGGCAAGTGAAGTCCACCTTGACTCGAACCAGAGTCAAGATGCCAGAGCACATATCCACA
 GTGAAACTCTGTCTCACTCAATCCAGACACAGGGCTGTGGGAGGAGGAGGTGATTTCAAATTTGAAAATCAAG
 GAGGAACAAAAGAGAGACAGAACCTTCTGGTGGGCAACCTGGAGATCTGTGAGAGGAGGCTCTTTAACTGG
 ATGTTCTCTGAAAGCAGGCGGTGCTTTGTTAAAGTGAAGGCTACCGGAGTGAGAGGTTCTTGCTAGTGACAG
 ATCCAGGGGGTGTGATCTCCGTGATTAACTGGAGCTTAGAATCTGCTCTCTGCTCAACCTTAGGCGCTGGG
 CGCCTTTGACAGTGTCTACAGAGGCCCAAGCGGCGCTGTGTGCTGCTCTCTGTGATGACCACTCCCTGTATG
 CTAATCTGCTGCTGTGTTGGCAAGCTGGCTGGGGAGGAACTCAAGCAGTGGAGTCTTCTCTCTAAATCAAC
 CCAATTCGATTTGGCTCTCTCAGCCCTATCTCAACAACCTCACTACCTCGGACGGACCATGGAGATCCACG
 GGTAAACAAACAGCTTTCCAGATTAGCATGGCCAGGCCAAGGCCAATCAGCTGAGGAGGCAATGGGCCCA
 TCTATGCTTTGAGAACCTCCGGGCTATGTGAAGAGGCCACCCAGTGCAGCCCATTTCCGGTTCTACAGATTT
 GAGGGGATCGATATGACTACACACAGTCCCTTCAACGAAGATGACCTATGAGCTGGACTGAAGACTATCT
 GGCATGGTGCCCAAGCCGATGGGAATTCAGGGCTGCTATATCAAGTGAAGATTTGGGGCCACTGGAAGTGA
 ATGTGCGATCCCGCAACATGGGGGGCACTCATCGCGGACAGTGGGGAAGCTGTATGGAATCCGAGATGTGAGG
 AGCACTCGGGACAGGACAGCCCAATGTCTCAGCTGCTGTCTGGAAGTTCAGTGCAGTGGGATGCTCTATGA
 TCAGGAGCTGTGTGACCGCACCTGGTGAAGTCTATCCCCAGGGGCAAGTGGCGTGAGGCGCTGTGAACCCCA
 TGCTGATGAGTACCTGGTCAACCACTTGGCACTTGCAGTCAACAACGACACCCAGTGCAGTACACCTGCTGSCA
 CCTTGGACCCACTGGGCCACAACATGGCATCTACACTGTCACTGACAGGACCTGCACGGCCCAAGGAGAT
 CGGCTCGGGCGGTGCTTTGATGCGCATATCCATGCTCTCTCAGATCATGAAGCAATGTGGGAGTGGCC
 TCACTTCACTGTGTAGAGGCGAGTAGCGCCAGAGTGCCTCCAGTACTCTCAAGACACCCAGCCGACCC
 TCCCTCTGCTGAGCACTCTCAAGGAAGAGTGCCTCGAGGAGGACAGCGAGCGAGCGAGCGGGGTGGCCAGCG
 CAGGCTGAGCTGTGGGCTCTCTGAGATTTCTGAGACTTGTCTCAACAGCCCTGATCAACTAAGTTTGTGGT
 ACTTACCCCTCTTCTGCTCCTATTTCATGTGACAGCCATTGTGAGACTGATGACCAACACTGTCACTTGTGTAAT
 TTAAGCACTTCTGTTTCTGTAATTTGCTGTTTGTGTTCTCATGCTTTTACTTACTTGTGCCATGCTACTGA
 TTGGCAGCTGGCCCAACATGGCAATGAAGGCCCTTTGTGAACTGTTCTTTAAATGAAACAAAGAAATTT
 GGGCACTGGTAAACACTGACGCTTCACTGTACTTCAATTAAATGCCATTAATGCAAAATATCTCTCTCTT
 TTGTCATGGTTTGGCCACTCTGCAATGTGATAATCTGATGCTGAAGTCAAAATACCAATATAAAGCATAT
 TTCTTGGCCTTGTCTCAGGACATAGGCAAGCCCTGTATCATAGTTATCATATAAATGGTGGTGAATAAAG
 AATAAACAACAATACTTTACTTGAATGTAATAAATCTATTATTCTTCTGCTAAATTTGGAATCTAGTGC
 ACATTCAAAGTTAAGCTATTAAATATAGGGTGATCATAGTTCCCTTCAGCAAGTCTGAAAGAACATCTCGGT
 ATCCCAATACCAAGTTGCTAAGTGTATTGTACATTTCCCTTACCATTCGCTTTTGTCTGCTAGAAAC
 CCAGTGTAGCCAGGCGAGATCTCAATAAATGCATCTCTGTATTTCGAAAAA

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FIGURE 72

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPSIFAKPADTLESPGEWTTWFNI
DYPGGKG DYERLDAIRFYYGDRVCARPLRLEARTTDWTPAGSTGQVHGS PREGFWCLNREQ
RPGQNC SNYTVRFLCPPGSLRRDTERIWSFWSKCSAACGQTGVQTRTRICLAEMVSLCS
EASEEGQHCMGQDCTACDLTCMPGQVNADCDACMCQDFMLHGAVSLPGGAPASGAAYLLTK
TPKLLTQTDS DGRFRIPGLCPDGK SILKITKVKFAPIVL TMPKTS LKAATIKAEFVRAETPY
MVMNPETKARRAGQSVSLCCKATGKPRPDKYFWYHNDTLLDPSLYKHESKLVLRLQHQAG
EYFCKAQSDAGAVKSKVAQLIVTASDETPCNPVPESYLIRLPHDCFQ NATNSFY YDVGRCPV
KTCAGQQDNGIRCDAYQNC CGISKTEEREIQCSGYTLPTKVAKECSCQRC TETR SIVRGRV
SAADNGEPMRFGHVYMGNSRVSM TGYKGTFTLHVPQDTERLVLTFVDRLQKFVNTTKVLPFN
KKGSAVFHEIKMLRRKEPITLEAMETNIIPLGEVVGEDPMAELEIPSR SFYRQNGE PYIGKV
KASVTFLDP RNISTATAAQTDLNF INDEGDTFPLRTYGMFSVD FRDEVTSEPLNAGKV KVLH
DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLFNL
DVPESRRCFVKVRAYR SERFLPSEQIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGA
CVPAFCDQSPDAYSAYVLASLAGEELQAVESSPKFNPNAIGVPQPYLNKLN YRRTDHEDPR
VKKTAFAQISMAKPRPNSAEESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDNTVPFN
EDDPMSWTE DYLAWWPKPMEFRACYIKVKIVGPLEVNVR SRNMGGTHRRTVGKLYGIRDVRS
TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTL VKVIPQGS CRRASVNPMLHEYLVNHLPLAV
NNDTSEYTM LAPLDPLGHNYGIYTVTDQDPRTAKEIALGRCFDGTS DGSSRIMKSNVGVALT
FNCVERQVGRQSAFYQLQSTPAQSPAAGTVQGRVPSRRQQRASRGGQRQGGVVASLRFPRVA
QQPLIN

FIGURE 73

CTGCAAGTGTGTTAACGCCCTAACACACAAGTATGTTAGGCTTCCACCAAAGTCTCTCAATATACCTGAATACGCAC
 AATATCTTAACTCTTCATATTTGGTTTTGGGATCTGCTTTGAGGTCCCATCTTCATTTAAAAAAAATACAGAG
 ACCTACCTACCGGTACGGATACATACATATGTGTATATATGTAAACTAGACAAAGATCGCAGATCATAAAGC
 AAGCTCTGCTTTAGTTTCCAAGAAGATTACAAAGAATTTAGAGATGTTGTTGTCGAAGATCCCTGTCGATTGATG
 CCCTTTGGGTTACGGTGTCTCAGTGTGTCAGCCCTACCCCTTTGGTTGTTGGGACATTTAGATTGTTGTAAGACT
 CAGATTTACACGGAAGAGGAAAGTTTGGGATTACATGGCCTGCCAGCCGGAATCCACGGACATGACAAAATA
 TCTGAAAGTGAAACTCGATCTCCGGATATTACCTGTGGAGACCTCTGAGACGTTCTGTGCAATGGGCAATC
 CCTACATGTGCAATAATGAGTGTGATGCGAGTACCCCTGAGCTGGCACACCCCTGAGCTGATGTTTGATTTT
 GAAGGAAGACATCCCTCCACATTTTGGCAGTCTGCCACTTGGAGGAGTATCCCAAGCCTCTCCAGGTTAACAT
 CACTCTGCTTGGAGCAAAACCATTTAGCTAACAGACAACATAGTTATTACCTTTGAATCTGGGCGTCCAGACC
 AAATGATCCTGGAGAAGTCTCTCGATTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTA
 GATGCTTTTACATGGATCCTAAATCCGTGAAGGATTTATCAGCAGATACGGTCTTAGAAATCATTTGCACAGA
 AGAGTACTCAACAGGGTATACACAAATAGCAAAATAATCCACTTTGAAATCAAAGACAGGTTGCGCTTTTTG
 CTGGACCTCGCCTACGCAATATGGCTTCCCTCTACGGACAGCTGGATACACCAAGAACTCAGAGATTTCTTT
 ACAGTACAGACCTGAGGATAAGGCTGTTAAGACCAGCCGTGGGGAATATTTGATAGATGAGCTACACTTGGC
 ACGCTACTTTTACGCGATCTCAGACATAAAGGTGCGAGGAAGGTGCAAGTGTAACTCTCCATGCCACTGTATGTG
 TGTATGACAAACAGCAAAATGACATCGCAATGTGAGCACAACTACAGGTCAGACTGTGGGAAATGCAAGAAG
 AATTATCAGGGCCGACCTTGGAGTCCAGGCTCCTATCTCCCATCCCCAAAGGCACTGCAATACCTGTATCCC
 CAGTATTTCCAGTATTTGTTACGAATGTCTGCGACACAGAGCTCTGCACTGCCAGAACGGAGGGACGTGCCACA
 ACAACGTGCGCTGCTGTGCCCGGCCGCATACACGGGCATCCTCTGCAGAAAGCTGCGGTGCGAGGAGGCTGGC
 AGCTGCGGCTCCGACTCTGGCCAGGCGCGCCCCCGCACGGCACCCACGCGCTGCTGCTGCTGACACGCTGCT
 GGGAACCGCCACGCCCTGTTTCTAGGTTGTCACCTCCAGCCACACCGGACGGGCTGTGCCGTGGGGAAGCA
 GACACACCCAAACATTTGCTACTAACAATAGGAAACACACACATACAGACACCCCACTCAGACAGTGTACAAA
 CTAAGAAGGCCCTAACTGAACCTAAGCCATATTTATCACCCGTGGACAGCACATCCGAGTCAAGACTGTTAATTTT
 TGAATCCAGAGGAGTTGGCAGCTGTTGATATTTATCACTGCAAAATCACATTGCCAGCTGCAGAGCATATTTGTGGA
 TTGAAAGGCTGCGACAGCCCCCAACAGGAAAGACAAAAACAACAAATCAACCGACCTAAAAACATTTGGC
 TACTCTAGCGTGGTGCGCCCTAGTACGACTCCGCCAGTGTGTGGACCAACCAAAATAGCATTCTTTGCTGTGAG
 GTGCATTGTGGGCATTAAGGAAATCTGTTACAGCTGCCATATTGGCCTGCTCCGTCCTGAAATCCCTTCCAAAC
 CTGTGCTTTAGTGAACGTTGCTCTGTAACCTCGTTGGTTGAAAGATTCTTTGCTGATGTTAGTGATGCCACA
 TGTGTAACAGCCCCCTCTAAAAGCGCAAGCCAGTCAATACCCCTGTATATCTTAGCAGCACTGAGTCCAGTGGCA
 GCACACACCCCATATACAGAGTGGCTATAGGAAAAAGAAAGTGTATCTATCCTTTTGATTCAAATGAAGTT
 ATTTTTCTTGAACCTACTGTAATATGTAGATTTTTGTATTATTGCCAAITGATTTACAGACAATCTGTTAAT
 GTATCTAATTCGAATCAGCAAAGACTGACATTTTATTTTGTCTCTTTCTGTTCTGTTTGTGTTTCACTGTGCAGA
 GATTTCTCTGTAAGGGCAACGAACGTGCTGGCATCAAAGAATATCAGTTTACATATATAACAAGTGAATAAGA
 TTCCACCAAGGACATTTCAAATGTTTCTTGTGCTTTAACTGGAAGATTAAAGAATAAAAACTCCTGCA
 TAAACGATTTCCAGAAATTTGTATTGCAATTTCTTAAGATGAAAGGAACAGCGCACCAAGCAGTTTCACACTCACT
 TTACTGATTTCTGTGGGACTGAGTACATTTAGTCCAGGTAAGATTTAGTCCAGGAAGATGGATTGATGTTCACT
 AGCTTGGACAACCTCTGCAAAATATGAGACTATTTCCACTTGGGAAAAATACAAACAGCAAAAAA
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FIGURE 74

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPELMFD FEGRHPSTFWQSATWK
EYPKPLQVNITLSWSKTIELTDNIVITFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAF
HMDPKSVKDLSQHTVLEI ICTEEYSTGYTTNSKIIHFEIKDRFALFAGPRLRNMASLYGQLD
TTKKLRDFFTVDLRI RLLRP AVGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN
SKLTCECEHNTTGPD CGKCKKNYQGRPWSPGSYLP I PKGTANTCIPSISSIGTNVCDNELLH
CQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQGAPPHGTPALLLLTTLLGTAS
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FIGURE 75

CCCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGGTGCGGCTAAGATTGCTGAGGAGGCGG
CGGGTAGCTGGCAGGCGCCGACTTCCGAAGGCCGCCGTCCGGGCGAGGTGTCTCATGACTT
CTCTTGTGGACCATGTCCGTGATCTTTTTTGCCTGCGTGCTACGGGTAAGGGATGGACTGCC
CCTCTCAGCCTCTACTGATTTTTACCACACCCAAGATTTTTTGAATGGAGGAGACGGCTCA
AGAGTTTAGCCTTGGCACTGGCCAGTATCCAGGTCGAGGTTCTGCAGAAGGTTGTGACTTT
AGTATACATTTTTCTTCTTTCCGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCC
AGCAGCCATGGCCTTCTGCTTCCCTGGAGACCCTGTGGTGGGAATTCACAGCTTCCTATGACA
CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTCAG
AAAGTGAAGTGGCATTTTAACTATGTAAGTTCCTCTCAGATGGAGTGCAGCTTGGAAAAAT
TCAGGAGGAGCTCAAGTTCAGCCTCCAGCGGTTCTCACTCTGGAGGACACAGATGTGGCAA
ATGGGGTGATGAATGGTCACACACCGATGCACTTGGAGCCTGCTCCTAATTTCCGAATGGAA
CCAGTGACAGCCCTGGGTATCCTCTCCCTATTCTCAACATCATGTGTGCTGCCCTGAATCT
CATTTCAGGAGTTCACCTTGCAACATTCTTTACAGGATCCAAGGAGCTGGTTCTGCTGGT
TGGACCAAACCTCGTGAGCCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT
CCGGGAGCAGTGATGTCAAACCTTCTGCTGCTGGGGAAATCTCATCAGCAGGGAGCCTGTGGA
AAAGGGCATGTCAAGTGAATCTGGGAATGGCTGGATTGCGAAACATCTGCCCATGTGTATTG
ATGGCAGAGCTGTTGCCCAAGCGCCTTTTATTTAGGGTAAAATTAACAAATCCATTCTAT
TCCTCTGACCCATGCTTAGTACATATGACCTTTAACCCTTACATTTATATGATTCTGGGGTT
GCTTCAGAAGTGTATTTTATGAATCATTATATGATTTGATCCCCCAGGATTCTATTTTGT
TTAATGGGCTTTTCTACTAAAAGCATAAAATACTGAGGCTGATTTAGTCAGGGCAAAACCAT
TTACTTTACATATTCGTTTTCAATACTTGCTGTTTCATGTTACACAAGCTTCTTACGGTTTTTC
TTGTAACAATAAATATTTTGAATAAATAATGGGTACATTTTAAACAACTCAGTAGTACAACC
TAACTTGTATAAAAGTGTGTAAAAATGTATAGCCATTTATATCCTATGTATAAATTAAATG
AGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTTTATTAAAAAAAAAAAAAAAAAAAAA
AAAAAG

FIGURE 76

MSVIFFACVVRVDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFSIHF
SSFGDVACMAICSCQCPAAMAFCFLETLWWEFTASYD'TTCIGLASRPYAFLEFDSIIQVKVK
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTA
LGILSLILNIMCAALNLRGVHLAEHSLQDPRSWFCWLQDTS

FIGURE 77

TGCTTCTCTGGAGACCTGTGGTGGGAATTCACAGCTTCNTATGACACTACCTGCATTGGCNT
 AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTAGAAAGTGAAGTGGCATT
 TTAACATATGTAAGTTCCTNTCAGATGGAGTGCAGCTTGAAAAAATTCAGGAGGAGCTCAAG
 TTGCAGCCTCCAGCGTTTCTCANTATGGAGGACACAGATGTGGCAAATGGGGT

CTCAGCGGCGCTTCTCTCGTAGCGAGCCTAGTGGCGGGTGTTTGCATTGAAACGTGAGCGCGA
CCCCGACCTTTAAAGAGTGGGGAGCAAGAGGGAGGACAGGCCCTTTAAAAAGCAGGCGGGTGGTG
CTGTGCCCTTTTAAAGGCGGGGCTCCGAGCAGTGTATCTGAGCCAGACTGCCCGGATTT
TCTGTGCGAGGCTCGGAGGGAAGGCCCTTAGGCTGGGCTGGGTGCTTGGCGGCGGCGGCTT
CCTCCCCGCTCGTCTCTCCCGGGCCGAGGACCTCGGCTTGAGTCACTGCTGAGCAGAGAT**A**
TGGAAGCACTGACTACAGAGTGCTATCCGTGCGGAGAAGCAGTATTCCACGAGAGGATCCGG
GAGTGATTATTATACAACATCTCTGTTTGAACACTGTACATCTCTGCCACATCTTCTGAG
CCGCTTCAAGAAGCCTGCTGAGTTCAACCACAGTGGATGATGAAGATGCCACCGTCAACAAGA
TTGCGCTCGAGCTGTGCACCTTTACCTTGGCAATTGCCCTGGGTGCTGTCTGCTCTGCC
TTCCTCCATCATCAGCAATAGGTTGCTGCTCTCCCTGCTCGGAACACTACATCACTCAGTGGCT
CAACGGCTCCCTCATCATGATGGCTCTTGGAACTTGTTTTTCTCTTCCCCAACCTGTCCCTCA
TCTTCTCATGCCCCTTTGCAATTTTCTTCACTGAGTCTGAGGGCTTTGCTGGCTCGAGAAAG
GGTGCTCTGGCGGGCTATAGACAGTGGTGATGTTGATGCTCTCACTGCTGCTGTGCT
AGGATAGGTTGGGTGGGCATCAGCCATTGTGGACAAGAACAAGGCCAACAGAGAGTCACTCT
ATGACTTTTGGGAGTACTATCTCCCTACTCTACTCATGATCATCTCTTCTTGGGTTCTG
CTGCTCTGTGTGTACTCTCACTGGGTCTGCGCCGATGTTCTCGCTCACTGGGAAGTGCT
AGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGAGCAGCTGTACTGCTCAGCCTTTGAGGAGG
CAGCCCTGACCCGCGAGGATCTGTAATCTTACTTCTGCTGGCTGGCTTTAGACATGGAGCT
CTACACAGACAGGTCCTGGCTCTGCAGACACAGAGGGTCTGCTGGAAGAAGGCGAAGGC
TTCAGCTGGCAACGGAACCTGGGCTACCCCTGGCTATGCTGTGCTTGTGCTGGTGCTGACGG
GCCTGTCTGTGCTCATTTGTGGCCATCCACATCTCGGAGCTGCTCATGATGAGGCTGCCAT
CCCCGAGGCAATGCAGGGTACCTCCTTAGGCCAGGTCTCTCTTCCAAGCTGGGCTCTTTGG
TGCGCTCATTCAGTTGTACTCATCTCTTTTAACTAATGGTGTCTCAGTTGTGGGCTCTATA
GCTCTCACTCTCTCCGAGAGCTGCGGCCAGATGGCAGCAGCACTGCCATGACGCAAGTAAT
GGGAACCTGTCTGTCTCTGCTCTGGTCTAAGTCACTGACATTTCTGTTCTCTGCAACCTTGG
GCTACTCGCTTTGACTGTGGGTGATTTGGAGCGCTTCAACTGGCTGGGCAATTTCTACA
TTGTGTTCTCTACAAACGACGCTTTTGCAGGCCCTACGACCTGTCTGTTGTAAGACATTC
ACTGCAGCTGTGCGGCGAGAGCTGATCGGGCTTGGGCTGGACAGACTGCCGCTGCCCT
CTCCGGTTTCCCCAGGCATCTAGGAAGACCCAGACCA**TGA**CTCTCAGCTGGGGTGGGA
AGGAAAAAATCGGACATGCCATCTGCTGCTAGGCCTGGAGGGAAGCCCAAGGCTACTTGG
ACCTCAGGACCTGGAATCTGAGAGGGTGGGTGGCAGAGGGAGCGGCATCTGCATATT
GATAATCTGAGCCAGAGTTTGGGACAGAGACCTCTGCTTTTCCATACTTAAGTGTGGCT
CAGCATGGGATAGGGTGTGGGTGACTGGGTCTAGCCCTGATCCCAAACTGTTTACATACAT
ATCTGCTCACTGCTGTTCTGGGCCATCCCCATAGCCATGTTTACATGATTGATGCAAT
AGGGTGGGTGAGGGCAGGGAAGGACTGGGCCAGGGCAGGCTCGGAGATAGATTGTCTCC
CTTGCTCTGGCCAGCAGAGCCTAAGCACTGTGTATCTCGAGGGGCTTTGGACCACTG
AAAGAACAGGGGATAGGGAGGAGGAGGCTTCAGCCATCAGCAATAAGTTGATCCAGGGA
AAAAAA

FIGURE 79

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATVNK
IALELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYIIQWLNGSLIHGLWNLVFLFPNLSL
IFLMPFAYFFTESEGFAGSRKGVLRVYETVVMLMLLTLLVLGMVWVASAIVDKNKANRESL
YDFWEYYLPYLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEEQLYCSAFEE
AALTRRICNPTSCWLPLDMELLHRQVLALQTRVLEKRRKASAWQRNLGYPLAMLCLLVLT
GLSVLIVAIHILELLIDEAAMPGRMQGTSLGQVSFSKLGSGFAVIQVVLI FYLMVSSVVG FY
SSPLFRSLRPRWHDAMTQII GNCVCLLVSSALPVFSRTLGLTRFDLLGDFGRFNWLG NFY
IVFLYNAAFAGLTTCLVKTF TA AVRAELIRAFGLDRLPLPVSGFPQASRKTQH Q

GGCTGCCGAGGGAAGGCCCTTGGGTTGGTCTTGGTTGCTTGGCGGCGGCGGNTTCNTCCCC
GCTCGTCTCTCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGTGTA
TTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTC
AAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCG

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAACGAGGCGGTGGTGC
CTGCCCTTTAAGGGCGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTTTC
TGTCGCAGGTGCGAGGAAAGGCCCTAGGCTGGGTCTGGTGCTTGGCGGCGGCGGCTTCCT
CCCCGTTGTNTCCCCGGGCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA
AGCACCTGACTACGAAGTGTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT
GTATTATATCAACACTTCTGTTTGAACACTGTACATCNTCTGCCACATCTTCTTGACCCGC
TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC
GCTCGAGCTGTGCACCTTTACCCTGGCAATTGCCCTGGGTGCTGTCTGCTCCTGCCCTTCT
CCATCATCAGCAATGAGGTGCTGCACTCCC

FIGURE 82

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTT
GGAATTGAGGAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTTCATGCTGCTGT
GGGTGATATTACTGGTCCTGGCTCCTGTCAGTGGACAGTTTGCAAGGACACCCAGGCCCAT
ATTTTCCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCCCTCACTTGCAA
GGGATTTTCGCTTCTACTCACACAGAAAACAAAATGGTACCATCGGTACCTTGGGAAAGAAA
TACTAAGAGAAACCCAGACAATATCCTTGAGGTTTCAGGAATCTGGAGAGTACAGATGCCAG
GCCCAGGGCTCCCTCTCAGTAGCCCTGTGCACCTGGATTTTCTTCAGAGATGGGATTTCC
TCATGCTGCCCAGGCTAATGTTGAACTCCTGGGCTCAAGTGATCTGCTCACCTTAGGCCTCTC
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGAC
TCTGTGGTTCTGAGGTGCCGGGCAAGGCGGAAGTAACACTGAATAATACTATTTACAAGAA
TGATAATGTCTTGGCATTCTTAATAAAAGAACTGACTTCCAAAAAAAAAAAAAAAAAAAAA
AAA

FIGURE 84

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCGGTGT
GAGGCGGCCCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGGCGCGGAGGAGGCTGTGAG
GAGTGTGTGGAACAGGACCCGGGACAGAGGAAC**CATGG**GCTCCGCAGAACCTGAGCACCTTT
GCCTGTGTGCTATACCTCATCGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTG
GGGGTGCCTCGAAGTGCCCTCTATAAAGGATATTTAAAAAGGCCTATAGGAACTAGCCCTGCA
GCTTCATCCCGACCGGAACCTGATGATCCACAAGCCCAGGAGAAATTCAGGATCTGGGTG
CTGCTTATGAGGTTCTGTCTAGATAGTGAGAAACGGAACAGTACGATACTTATGGTGAAGAA
GGATTAAGAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTACACTTCTTTGGGGATT
TGGTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCAGAGGAAGTGATA
TTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGT
AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTTGTGGCAAGAGAT
GCGGACCACCCAGCTGGGCCCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT
GCCCTAAATGTCAAACCTAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGT
AGAGACGGCATGGAGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTG
AGATTTACGGTTCGAATCAAAGTTGTCAAGCACCCAATATTTGAAAGGAGAGGAGATGATT
TGTACACAAATGTGACAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT
CACTTGGATGGTCACAAGGTACATATTTCCCGGGATAAGATCACCAAGGCCAGGAGCGAAGCT
ATGGAAGAAAGGGGAAGGGCTCCCCAACTTGACAACAACAATATCAAGGGCTCTTTGATAA
TCACTTTTGTATGTGGATTTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAA
CAGCTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATAT**TCA**GAGTG
AATAAAATTGGACTTTGTTTAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT
TTGTGTGTGTTTTTGTTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTTATCTAATGA
TCATCATGAATGAATAAGAGGGCTTAAGAATTTGTCCATTGTGCATTCGGAAGAAGTACC
AGCAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGCTGCCGCTGAGT
TTCAAGAATTAAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGA
GTTGTTAGCAATTTTCATTCAAATGCCAAGTGGAGAAGTCTGTTTTTAAATACATTTTGTG
TTATTTTTTA

FIGURE 85

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIKKAYRKALQLHPDRNPDDPQ
AQEKFQDLGAAYEVLSDSEKRKQYDITYGEEGLKDGHQSSHGDI FSHFFGDFGFMFGGTPRQQ
DRNIPRGSDIIVDLEVLTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPRFQ
MTQEVVCDECFNVKLVNEERTLEVEIEPGVRDGMETPFFIGEGEPHVDGEPGDLRFRIKVVKH
PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGLPNFD
NNNIKGLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

FIGURE 86

TGGGACCAGGGAACCCCGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA
GCGGCGGGCGGAGGAGGTTTTTGAGGATTTTTTGAACAGGACCCGGACAGAGGAACCATGGTT
CCGCAGAACNTGAGCACNTTTTGCCTGTTGNTGNTATACTTCATCGGGGCGGTGATTGCCGG
ACGAGATTTNTATAAGATTTTGGGGTGCCNGAAGTGCCTTNTATAAAGGATATTAAAAAGG
CCTATAGGAAACTAGCCCTGCAGNTTATCCCGACCGGAACCCTGATGATCCACAAGCCCAG
GAGAAATTCAGGATTTGGGTGCTGCTTATGAGGTTNTGTCAGATAGTGAGAAACGGAAACA
GTACGATAATTATGTTGAAGAAGGATTAAGATGGTNATCAGAGCTCCCATGGAGACATTT
TTTCACACTTNTTTGGGGATTTTGGTTTCATGTTTGGAGGAACCCCTNGTCAGCAAGACAGA
AATATTCCAAGAG

TGGGACCAGGGAACCCCGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA

FIGURE 87

GGCACGAGGCGGCGGGGAGTGC GCGGGATGCGCCCCGGGAGCCACAGCCTGAGGCCCTCAGGT
CTCTGCAGGTGTCGTGGAGGAACCTAGCACCTGCCATCCTCTTCCCCAATTTGCCACTTCCA
GCAGCTTTAGCCCATGAGGAGGATGTGACCGGGACTGAGTCAGGAGCCCTCTGGAAGC**ATGG**
AGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCATCTTTCTGGCTTCGTTTGCAGCC
TTGGTGCTGGTTTGCAGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGCGCTATGATT
TAAGCCCATGTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC
TGGACGATGTCTGTTATCACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC
GAAGATGCCTCGGGTCTCATGTCCCACTGCATTGCCATCTTGAAGATTTGTCACACTCTGAC
AGAGAAGCTTGTTGCCATGACAATGGGCTCTGGGGCCAAGATGAAGACTTCAGCCAGTGTCA
GCGACATCATTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG
TACCTCCGTTGGACCCCAAACCTCTGGACGCACGGACGACTGCCCTGCTCCTGTCTGTTCAG
TCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCTTGACTGGATTGACC
AGTCTCTGTGGCTGCTGAGGAGCATTGGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAG
CCAGATAAAGGCCTCCAGGCCCTGAAGGCTTCCTGCAGGAGCAGTCTGCAATTT**TAGT**GCCT
ACAGGCCAGCAGCTAGCCATGAAGGCCCTGCCGCCATCCCTGGATGGCTCAGCTTAGCCTT
CTACTTTTCCCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTCAGCTGTGTGTGCATAG
TAAAGCAGGAGATCCCCGTAGTTTATGCCTCTTTTGCAGTTGCAAACTGTGGCTGGTGAGT
GGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACTCTCTGCAAGAGGAGTATTGAAAA
CTGGTGGACTGTGAGCTTTTATTTAGCTCACCTAGTGTTCCTAAGAAAATTGAGCCACCGTCT
AAGAAATCAAGAGGTTTCACATTAAAATTAGAATTTCTGGCCTCTCTCGATCGGTGAGAATG
TGTGGCAATTCTGATCTGCATTTTTCAGAAGAGGACAATCAATTGAAACTAAGTAGGGGTTTC
TTCTTTTGGCAAGACTTGTACTCTCTCACCTGGCCTGTTTCAATTTATTTGTATTATCTGCCT
GGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTTGCAGGTTTGGGTTTGAAGCTGAGGAACT
ACAAAGTTGATGATTTCTTTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTG
GATAGTAAATTTATACTTATGTTTCCCTCAAAAAAAAAAAAAA

FIGURE 88

METVTVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSSEL
 ELDDVVITNPHIEAILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKMKTAS
 VSDIIVAKRISPRVDDVVKSMYPLDPKLLDARTTALLSVSHLVLVTRNACHLTGGLDWI
 DQSLSAEEHLEVLREAALASEPDKGLPGPEGFLQEQSAI

FIGURE 89

GCTTCATTTCTCCCGACTCAGCTTCCCACCCTGGGCTTTCCGAGGTGCTTTCGCCGCTGTC
CCACCACTGCAGCCATGATCTCCTTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGA
TTTGGAGTGTTTTCTGTCTTTGGAATGATTCTCTTTTTTGACAAAGCACTACTGGCTAT
TGGAATGTTTTATTGTAGCCGGCTTGGCTTTTGTAATTGGTTTAGAAAGAACATTCAGAT
TCTTCTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTCTGGTGGTGATTTGTAGTC
CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTCTCTTGTTCAG
GGGCTTCTTCTGTCTGTTGTTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAAT
TTACCTGGAATTAGATCATTGTAGATAAAGTTGGAGAAAGCAACAATATGGTATTACAACA
AGTGAATTTGAAGACTCATTTAAAAATATTGTGTTATTTATAAAGTCATTTGAAGAATATTCA
GCACAAAATTAAATTACATGAAATAGCTTGTAAATGTTCTTTACAGGAGTTTAAACGTATAG
CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAAAACAGGCCTCTACTCAAGTGA
ACTAAGAAGAAGTCAGCAAGCAAACAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAA
ACTCTTGAAGGCTATTTGTGTTGTTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAA
CTGTGGTGCCTGTTTCTTTTCTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCT
TTTTAGAAGTGTCCACTGCAATGGCAAAAATATTTCCAGTTGCACTGTATCTCTGGAAGTGA
TGCATGAATTCGATTGGATTGTGTCATTTTAAAGTATTAAACCAAGGAAACCCCAATTTTG
ATGTATGGATTACTTTTTTTTTGNGCNCAGGGCC

FIGURE 90

MISLTDTKQKIGMLTGFVFFLFFGMILFFDKALLAIGNVLVAVGLAFVIGLERTFRFFQK
 HKMKATGFFLGGVFFVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRVPVGLSLLNLPGI
 RSFVDKVGESNNMV

Important features:

Transmembrane domains:

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

FIGURE 91

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTTCCCGGCTTCATTTCTCCCGACTCAGCTTCCC
ACCNTGGGCTTTCCGAGGTGCTTTGCGCGCTGTCCCCACCACTGCAGCCATGATCTCCTTAA
CGGACACGCAGAAAATTGGAATGGGATTAACCGGATTGGAGTGTTTTCTGTTCCTTTGGA
ATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGAAATGTTTTATTTGTAGCCGGCTT
GGCTTTTGTAAATGGTTTAGAAAGAACATTCAGATTCTTCTCCAAAACATAAAATGAAAG
CTACAGGTTTTTTCTGGGTGGTGTATTTGTAGTCCTTATTGGTTGGCCTTTGATAGGCATG
ATCTTCGAAATTTATGGATTTTTTCTCTTGTTT

FIGURE 92

GGACACGAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAAGGCTGCCAGGAAGGAGACGCCTTCTCAGTCTCGGATCTTTCTTCTTCTGGAATCTTTGACTGTGGGTAGTTATTTATTTCTGAATAAGACGCTCCACGCATC**CATG**CACTCGCGGGACTGCTGAAGTCTCAGTTCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGCCTCAGGGCTAATCATCAACACCATTCAGCTCTTCACTCTCTCCTCTGCCCCATTAAACAAGCAGCTCTTCCGGAAGATCAACTGCAGACTGTCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGTCGGGCACGGAATGCACCATCTTCAACGACCCGCGCGCTACCTCAAGTATGGGAAGGAAAAAGCCATCGTGGTTCTCAACCACAAGTTTGAAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGACGCTTTGGGCTGTTAGGGGGCTCCAAGTCTTGCCCAAGAAAGAGCTGGCCTATGTCCCAATTATCGGCTGGATGTGGTACTTCACCGAGATGGTCTTCTGTTCCGCAAGTGGGAGCAGGATCGCAAGACGGTTGCCACCAAGTTTGACGACCTCCGGGACTACCCCGAGAAGTATTTTTTCTTGATTTCACTGTGAGGGCACACGGTTCACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCCAGGGCCAAAGGGCTGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATCACCGTGAGGAGCTTGAGAAATGTAGTTTCAGCTGTATATGACTGTACACTCAATTTAGAAAATAATGAAAATCCAACACTGCTGGGAGTCTAAACGGAAAGAAATACCATGCAGATTTGTATGTTAGGAGGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCTGGCTGCACAAGCTCTACCAGGAGAAGGATGCCCTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCCGAGACGCCCATGGTGCCCCCGCGCGCCCTGGACCTCGTGAACCTGGCTGTTTTGGGCCCTCGCTGGTGCTCTACCCTTTCTTCCAGTTCCTGGTCAGCATGATCAGGAGCGGGTCTTCCCTGACGCTGGCCAGCTTCATCTCGTCTTCTTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGTGACGGAATTTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAAACTGAATGACT**G**ACTCAGGGAGGTGTACCATCCGAAGGGAACCTTGGGGAACCTGGTGGCCTCTGCATATCCTCCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCCCTGCTGGGCACGGCGGAAGTCACGACCTTCCAGCCAGGGAGTCTGGTCTCAAGCCGGATGGGGAGGAAGATGTTTTGTAATCTTTTCCCCCATGTGCTTTAGTGGGCTTTGGTTTTCTTTTGTGCGAGTGTGTGTGAGAATGGCTGTGTGGTGAGTGTGAACCTTGTCTGTGATCATAGAAAGGGTATTTTAGGCTGCAGGGGAGGGCAGGGCTGGGGACCGAAGGGGACAAGTTCCCTTTTCATCCTTTGGTGCTGAGTCTTCTGTAAACCTTGGTTGCCAGAGATAAAGTGAAAAGTGCTTTAGGTGAGATGACTAAATTATGCCTCAAGAAAAAAAATTAAGTGCTTTTCTGGGTCAAAAAAAAAAAAA

MDLAGLLKSQFLCHLVFCYVFIASGLIINTIQFLTLLLPINKQLFRKINCRLSYCISSQLV
MLEWWSGTECTIFTDPRAYLKYGKENAIVLVNHNKFEIDFLCGWSLSERFGLLGSKVLAKK
ELAYVPIIGMWMYFTEMVFCSRKWEQDRKTVATSLQHLRDYPEKYFFLIHCEGTRFTEKKHE
ISMQVARAKGLPRLKHLLPRTKGFAITVRSLRNVVSAYVDCTLNFRNNENPTLLGVLNGKK
YHADLYVRRIPLEDIPEDDDECSAWLHKLYQEKFQEEYYRTGTFPETPMVPPRRPWTLVN
WLFWASLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASGVWRMIGVTEIDKGSAYGNSDS
KQKLN

FIGURE 94

CTGAGGCGGCGGTAGCA**ATG**AGAGGGGAGAGTACGTGCGGCGGTGCTCTCGGGCTTTGTGCTCG
GCGCACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTTGGGGAA
GTAAAAGGTGAAGCCAAGAACAGCATTACTGATTCCCAAAATGGATGATGTTGAAGTTGTTTA
TACAATTGACATTACAGAAATATATTCATGCTATCAGCTTTTTAGCTTTTATAATTCTTCAG
GCGAAGTAAATGAGCAAGCACTGAAGAAAAATATATCAAAATGTCAAAAAGAAATGTGGTAGGT
TGGTACAAATTCGTCGTCATTAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAA
AAACTTGCAGGAGCATTTTTCAAACCAAGACCTTGTTTTTCTGCTATTAAACCAAGTATAA
TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAAACCTCAAAAAGGACTT
TTTCACAGGGTACCTTTAGTGGTTGCCAATCTGGGCATGTCTGAACAAGTGGGTTATAAAAC
TGTATCAGGTTCTGTATGTCCACTGGTTTTAGCCGAGCAGTACAACACACAGCTCTAAAT
TTTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAAATGAAATGTATGCTTCATTA
CAAGAGGAATTAAGAGTATATGCAAAAAAGTGAAGACAGTGAAACAGCAGTAGATAAACT
AGTAAAGGATGTAAACAGATTAAACAGAGAAATTGAGAAAAGGAGAGGAGCACAGATTGAG
CAGCAAGAGAGAAGAACATCCAAAAAGACCCCTCAGGAGAACATTTTTCTTTGTGAGGCATTA
CGGACCTTTTTTCCAAATTTCTGAATTTCTTCATTATGTTATGTCTTTAAAAAATAGACA
TGTTTCTAAAAGTAGCTGTAACATAACCACCATCTCGATGTAGTAGACAATCTGACCTTAA
TGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAAGCAT
AAAGCCTTAGACTTAGATGACAGATGGCAATTCAGAGATCTCGGTTGTTAGATACACAAGA
CAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCC
CAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTACGGTCTCCTACA
TTTT**TGAT**CCTTTTAACCTTACAAGGAGATTTTTTTATTTGGCTGATGGGTAAAGCCAAACAT
TTCTATTGTTTTTACTATGTTGAGTACTTGCAGTAAGTTCATTGTTTTTACTATGTTTAC
CTGTTTGCAGTAATACACAGATAACTCTTAGTGCATTACTTCACAAAGTACTTTTTCAAAC
ATCAGATGCTTTTATTTCAAACCTTTTTTTTACCTTTTCTACTAAGTTGTTGAGGGGAAGGCT
TACACAGACACATTCTTTAGAATTGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAA
TCCAGCACTTAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC
TGGGCAACGTATTGAGACCATGTCTATTAAAAAATAAAATGAAAAGCAAGAATAGCCTTAT
TTTCAAAATATGGAAGAAATTTATATGAAATTTATCTGAGTCATTAATAATTCTCCTTAAG
TGATACTTTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCA
ATAAATTGCAAAACATCATCTAAATTTAAAAAATAAAAAAAAAAAAAAAAAAAAAA

MEGESTSAVLSGFVLGALAFQHLNLTSDTEGFLLGEVKGEAKNSITDSQMDDDEVVYITIDIQ
KYIPCYQLFSFYNSSGSEVNEQALKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEH
FSNQDLVFLLLTPSIITESCSTHRLHSLYKPKGLFHRVPLVLANLGMSEQLGYKTVSGSC
MSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVN
RLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSS
CNYNHHLDVVDNLTLMEHTDIPEASPASTPQIIKHKALDLDDRWFKRSRLDLDQDKRSKA
NTGSSNQDKASKMSSPETDEEIEKMKGFGEYSRSPTF

FIGURE 96

GGCAGACCCGCGCGGAGGGGACAGATCAGCCGAGCCGAGTCCAGCCGAGCAGCGGACCAGCGCAGGGCAGC
 CCAAGCAGCGCGCAGCGAACGCCCGCCGCCGCCACACCCCTCTGCGGTCCCCGCGGCGCCTGCCACCCCTTCCCT
 CCTTCCCGCGCTCCCGGCTGCGCGGCCAGTCAGCTTGCCGGTTGCTGCCCCGCGAAACCCGAGGTCAACA
 GCCCGCGCTCTGCTTCCCTGGCGCGCGCGCCCTCCACGCCCTCCTTCTCCCTTGGCCCGGCGCTGGCACC
 GGGGACCGTTGCCCTGACGCGAGGCCAGCTCTACTTTTCGCCCGCGCTCTCTCCGCCCTGCTCGCCTCTTCCAC
 CAACTCCAACCTCTTCCCTCCAGCTCCACTCGCTAGTCCCCGACTCCGCCAGCCCTCGGGCCGCTGCCGTAG
 CGCCGCTTCCCGTCCGGTCCCAAAGGTGGGAACCGCTCCGCCCGCGCCGACCATGGCAGCGTTCCGGCTTGCC
 CGCGCTTCTCTGCACCCCTGGCAGTGCTCAGCGCCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGG
 AAGTGCACGCTCTTACGTGTCCAAAGGCTTCAACAAGAACGATGCCCCCTCCACGAGATCAACGGTGATCAT
 TTGAAGATCTGTCCCAGGGTTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCCTGCAAAAGTAAAGA
 TGATTTCAAAGTGTGGTCAGCGAACAGTGCAATCATTGCAAGCTGTCTTTGCTTACGTTACAAGAAGTTTG
 ATGAATTTCTCAAAGAACTACTTGAAATGCAGAGAAATCCCTGAATGATATGTTTGTGAAGACATATGGCCAT
 TTATACATGCAAAATTTGAGCTATTTAAAGATCTCTTCGTAGAGTTGAAACGTTACTACGTGGTGGGAAATGT
 GAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATGTTCCGCTTGGTGAACCTCCAGT
 ACCACTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCCT
 CGCAAAATTGAAGCTCCAGGTTACTCGTGTCTTTGTAGCAGCCGTACTTTTCGCTCAAGGCTTAGCGGTTCGCGG
 AGATGTCGTGAGCAAGGTCTCCGTGGTAAACCCACAGCCAGTGACCCATGCCCTGTTGAAGATGATCTACT
 GCTCCCACTGCGCGGCTCTCGTGACTGTGAAGCCATGTTACAACACTGCTCAAAACATCATGAGAGGCTGTTTG
 GCCAACCAAGGGATCTCGATTTTGAATGGAACAATTTCTATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGA
 GGGTCTTTCAACATGAAATCGGTATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAAG
 ATAATAGTGTTCAGTGCTCTCAGAAGGTTTTCCAGGGATGTGGACCCCCCAAGCCCTCCAGCTGGACGAATT
 TCTCGTTCCATCTCTGAAAGTGCCCTTCACTGCTCGCTTCAGACCACATCACCCCGAGGAACGCCCAACCAAGC
 AGCTGGCACTAGTTTGGACCGACTGGTTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATTTCTGCTCCT
 CCCTTCCGAGCAACGTTTGCACACGATGAGAGGATGGCTGAGGAAACGGCAATGAGGATGACTGTTGGAATGGG
 AAAGGCAAAAGCAGGTACCTGTTTGCAAGTACAGGAAATGGATAGCCCAACGAGGCAACAACCCAGAGGTCCA
 GGTTGACACAGCAACAGACATACCTGATCTTCTGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGA
 AGAATGCATACAATGGGAACGACGTGGACTTCTTTGATATCAGTGATGAAAGTAGTGGAGAAGGAAGTGGAAAT
 GGCTGTGAGTATCAGCAGTGCCCTTCAGAGTTTGACTACAAATGCCACTGACCATGCTGGGAAGAGTGCCAAATGA
 GAAAGCCGACAGTGCTGGTGTCCGCTCTGGGGCACAGGCCCTACCTCCTCACTGCTTCTGTCATCTGTGCTG
 TTATGCAGAGAGAGTGGAGATTAATTTCTCAAACTCTGAGAAAAAGTTTCTACAAAAGTTAAAGGCCACCAAGTT
 ATCACTTTTCTACCATCTAGTGACTTTGCTTTTAAATGAATGGACAACAATGTACAGTTTCTTACTATGTGGC
 CACTGGTTTAAAGAGTGCTGACTTTGTTTTCTCATTGAGTTTGGGAGGAAAAGGACTGTGCATTGAGTTGGT
 TCGTGCTCCCCAAACCATGTTAAACGTGGCTAACAGTGATAGTACAGAACTATAGTTAGTTGTGCAATTTGTGA
 TTTTATCACTTATTATTGTTTTGTATGTTTTTTTCTCATTTCGTTTGTGGGTTTTTTTTTCCAACCTGTGATCT
 CGCCTTGTTCTTACAAGCAAAACAGGGTCCCTTCTTGGCAGTAACATGTACGATTTTCTGAAATATTAATA
 GCTGTACAGAAGCAGTTTTATTATCATGTTATCTTATTAAGAAAAAGCCCAAAAGC

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFKNKDAPLHEINGDHLKICPQ
GSTCCSQEME EKYS LQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKS LNDMF
VKTYGHL YMQNSE LFKDLFVELKRYVVG NVNLE EMLNDFWARLLERMFR LVNSQYHFTDEY
LECVSKYTEQLKPF G DVPRKLKLQVTRAFVAARTFAQGLAVAGDVVSKVS VNPTAQCTHAL
LKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLDFEWN NFIDAMLMVAERLEGPFNIES
VMDPIDVKISDAIMNMQDNSVQVSQKV FQCGCPPKPLPAGRISR SISESAFSARFRPHHPPEE
RPTTAAGTSLDR LVTDVKEKLQAKKFWSLSPSNCNDERMAAGNGNEDDCWNGKGKSRYLE
AVTGNGLANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGE
GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

FIGURE 98

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT
GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAA
GCAACTTACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGC
TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCAC
AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGCCAAGAATGTGAGTGCAA
AGATTGGTTCCTGAGAGCCCCGAGAAGAAAATTCATGACAGTGTCTGGGCTGCCAAAGAAGC
AGTGCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACCAAGGCACCAAGCAG
AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAAACAATGTGAGCTAAGAAGCTT
TGCTCTGCCTTTGTAGGAGCTCTGAGCGCCCACTCTTCCAATTAACATTCTCAGCCAAGAA
GACAGTGAGCACACCTACCAGACACTCTTCTTCTCCACCTCACTCTCCCACTGTACCCACC
CCTAAATCATTCCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTGTTGCTCTC
TCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCTTACCCAGGCTTAGGCTT
AATTACCTGAAAGATTCCAGGAAACTGTAGCTTCCTAGCTAGTGTCAATTTAACCTTAAATGC
AATCAGGAAAGTAGCAACAGAAAGTCAATAAATATTTTTAAATGTCAAAAAAAAAAAAAAAAAA

FIGURE 99

A**ATG**GCTGTCTTAGTACTTCGCCTGACAGTTGTCTCTGGGACTGCTTGTCTTATTCTTGACCT
 GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA
 AAGCCAGACTTCCCCAATTCTTAAGCCTCCTGGGCACAGAGATCATTGAGAAATGCAGTCGA
 GTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA
 AACATTATCA**AAAGTGA**CATCCTCAGGACACCCCATGTGGCTCCTGGACAATCCAAGAGCA
 GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC
 TCCCAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAAACAGAACTATTTTGAACACC
 CTGACTGCATTTTGTCTTTAGAAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTG
 ATGGAGAGGAA

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FIGURE 101

MAVLVLRLTVVLGLLVLFILTCYADDKPDKPDDSGKDPKPDFPKFLSLLGTEIIENAVE
FILRSMRSRSTGFMEFDDNEGKHSSK

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FIGURE 102

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCT
CAGAGCTGGTCTGCCATGGACATCTCTGGTCCCCTCTCTGCAGCTGCTGGTGCTGCTTCTTAC
CCTGCCCCCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCCTGTGC AAAAGCTACTTCC
CCTACCTGATGGCCGTGCTGACTCCCAAGGCAACCGCAAGATGGAGAGCAAGAAACGGGAG
CTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGCCCTACTGGAGCTGGG
CTGCGGAACCGGAGCCAACCTTTCAGTTCTACCCACCGGCTGCAGGTCACCTGCCTAGACC
CAAATCCCCACTTTGAGAAGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT
GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT
GGTGGTCTGCACTCTGGTGTCTGTCTGTGTCAGAGCCCAAGGAAGTCTGCAGGAGGTCC
GGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTCTGGGAGCATGTGGCAGAACCATATGGA
AGCTGGGCCCTTCATGTGGCAGCAAGTTTTCGAGCCCACCTGGA AAACATTTGGGGATGGCTG
CTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAAGCGCCAGTTCTCCGAAATCCAATG
AACGACAGCCCCCTCCCTTGAAGTGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTC
AAACAATCTTTCCCAAGCTCCAAGGCACCTCATTTGCTCCTTCCCAGCCTCCAATTAGAACA
AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTTAGCAGAATGAGAGAAGACATT
CATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGCAATCTCTAACTTCAATC
CCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCAGGGAGGAAACACTAGGACCC
TGTTGTATCTCTAACTGCAAGTTTCTGGACTAGTCTCCAACGTTTGCCCTCCAATGTTGTC
CCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCCATGCGT
CTCTAGGAACGGTCAAAAAGTCATGGTGCTGCATCCCTGCCAAGCCCCCTGACCCTCT
CTCCCCACTACCACCTTCTTCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGGAT
GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTTTAATAAATAGACGA
AACCACG

FIGURE 103

MDILVPLLQLLVLLLTLPPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSQI
KGLTGASGKVALLELGC GTGANFQFYPPGCRVTC LDPNPHFEKFLTKSMAENRHLQYERFVV
APGEDMRQLADGSMDVVVCTLVLC SVQSPRKVLQEVRRLRPGGVLFFWEHVAEPYGSWAFM
WQQVFEP TWKHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWL PVGPHIMGKAVKQSF P
SSKALICSFPSLQLEQATHQPIYLPLRGT

FIGURE 104

GTGGGATTTATTTGAGTGC AAGATCGTTTTCTCAGTGGTGGTGG AAGTTGCCTCATCGCAGG
CAGATGTTGGGGCTTTGTCCGAACAGCTCCCCCTGCCAGCTTCTGTAGATAAGGGTTAAAA
ACTAATATTTATATGACAGAAGAAAAAGATGTCATTCCGTAAAGTAAACATCATCATCTTGG
TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATAACTTCCTCAGCTTGAGCAGTTTG
TTAAGGAATGAGGTTACAGATT CAGGAATTGTAGGGCCTCAACCTATAGACTTTGTCCCAA
TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATCTG
AAGACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATT CAGCACAACTCGCTCCAAT
GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATCTCCGGTCTGGCTCAACAG
TGATTCCTGAAAAGCATCAGATACAAAATTGTCAATTTTGACCTAAACTTTTGGAAGGAA
AAGTAAAGGAGGATCCTGACCAGGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTAC
TTGCCAATCTGGTTC CAGCGCAAAGAAGCCATATACATGGATGATGATGTAATTGTGCA
AGGTGATATCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAG
AAGATTGTGATT CAGCCTCTACTAAAGTTGTCATCCGTGGAGCAGGAAACAGTACAATTAC
ATTGGCTATCTTGACTATAAAAAGGAAAGAATT CGTAAGCTTTCCATGAAAGCCAGCACTTG
CTCATTTAATCCTGGAGTTTTTTGTTGCAAACCTGACGGAATGGAAACGACAGAATATAACTA
ACCAACTGGAAAAATGGATGAAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCCTGGCT
GGTAGCATCACACACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCGATCC
TATGTGGAATGTCCGCCACCTTGGTTCCAGTGCTGGAAAACGATATTCACCTCAGTTTGTA
AGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATAT
ACTGATGTTTGGGAAAAATGGTATATTTCCAGACCCAACAGGCAAATTC AACCTAATCCGAAG
ATATACCGAGATCTCAAACATAAAGTGAAACAGAATTGAACTGTAAGCAAGCATTTCTCAG
GAAGTCCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA
GCAAGCCATGAAAAAGATGTGTCAGCTAGGTAAAGATGACAACTGCCCTGCTGGCAGTC
AGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTTTTCTT
ACTACAATGCTGAATGACTGGAAAGAAGAACTGATATGGCTAGTT CAGCTAGCTGGTACAGA
TAATTCAAAACCTGCTGTTGGTTTTAATTTTGTAACTGTGGCCTGATCTGTAATAAAAACCT
ACATTTTTT

MSFRKVNIIILVLAVALFLLVLHNFSLSSLLRNEVTDSGIVGPQPIDFVPNALRHAVDGR
QEEIPVIVIAASEDRLGGAIAAINS IQHNTRSNVIFYIVTLNNTADHLRSLWNSDSLKSIRYK
IVNFDPKLLEGGVKEDPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDIVQGDILALYNT
ALKPGHAAAFSEDCDSASTKVIVIRGAGNQNYIGYLDYKKERIRKLSMAKSTCSFNPGVFVA
NLTEWKRQNI TNQLEKWMKLNVEEGLYSRTLGSITTPPLLIVFYQQHSTIDPMWNVRLGS
SAGKRYSPQFVKAALLHWNGHLKPWGR TASYTDVWEKWYIPDPTGKFNLI RRYTEISNIK

FIGURE 106

TGGTTTTTGCCCCATAAATTCCTCAGCTTGAGCAGTTTGTTAAGGAATGAGGTTACAGATT
CAGGAATTNTAGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT
GGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGGCCAT
TGCAGCTATAAACAGCATTTCAGCACAACACTCGNTCCAATGTGATTTTCTACATTGTTACTC
TCAACAATACAGCAGACCATNTCCGGTCCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA
TACAAAATTGTCAATTTTGACCCTAACTTTTGGAAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTCTACTTGCCAATTCTGGTTCCCAGCG
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTACGCCTCTAC
TAAAGTTGTCATCCGTGGAGCAGGAAA

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FIGURE 107

CGACGCTCTAGCGGTTACCGCTGCGGGCTGGCTGGGCGTAGTGGGGCTGCGCGGCTGCCACG
GAGCTAGAGGGCAAGTGTGCTCGGCCAGCGTGCAGGGAACGCGGGCGGCCAGACAACGGGC
TGGGCTCCGGGGCTGCGGCGCGGGCGCTGAGCTGGCAGGGCGGGTCCGGGCGCGGGCTGCA
TCCGCATCTCCTCCATCGCCTGCAGTAAGGGCGCGCGGCGAGCCTTTGAGGGGAACGACT
TGTCGGAGCCCTAACAGGGGTGTCTCTGAGCCTGGTGGGATCCCCGGAGCGTCACATCACT
TTCCGATCACTTCAAAGTGGTTAAAACTAATATTTATATGACAGAAGAAAAAGATGTCATT
CCGTAAAGTAAACATCATCATCTTGGTCCTGGGCTGTTGCTCTCTTCTTACTGGTTTTGCAC
CATAACTTCCTCAGCTTGAGGCAGTTTGTTAAGGAATGAGGTTACAGATTGAGGAATGTAG
GGCCTCAACCTATAGGACTTTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA
GGAGATTCTGTGGTCATCGCTGCATCTGAAGACAGGCTTGGGGGGGCCATTGCAGCTATAA
ACAGCATTGAGCACAACACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACA
GCAGACCATCTCCGCTCCTGGGCTCAACAGTGATTCCTGAAAAGCATCAGATACAAAATTG
TCAATTTTGACCCTAACTTTTGGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCC
ATGAAACCTTTAACCTTTGCAAGGTCTACTTGCCAATTCGGGTTCACAGCGCAAAGAAGG
CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCA
CTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTGAGCCTCTACTAAAGTTGT
CATCCGTGGAGCAGGAAACCAAGTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAA
TTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTAAATCCTGGAGTTTTTGTGCAAA
CTGACGGAATGGAACGACAGAATATACTAACCAACTGGAAAAATGGATGAACTCAATGT
AGAAGAGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAACACCTCCTCTGCTTATCG
TATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTTCCAGT
GCTGGAAAACGATATTACCTCAGTTTGTAAGGCTGCCAAGTTACTCCATTGGAATGGACA
TTTGAAGCCATGGGGAAGGACTGCTTCATATACTGATGTTTGGGGAAAAATGGTATATTCCA
GACCAACAGGCAAATTCACCTAATCCGAAGATATACCGAGATCTCAAACATAAAGTGAAA
CAGAATTTGAACTGTAAGCAAGCATTCTCAGGAAGTCTGGAAGATAGCATGCGTGGGAAG
TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGAAAAAGATGTGTGAGCTAG
GTAAAGATGACAACTGCCCTGTCTGGCAGTCAGCTTCCAGACAGACTATAGACTATAAAT
ATGTCCTCATCTGCCTTACCAAGTGTTTCTTACTACAATGCTGAATGACTGGAAGAAGAA
CTGATATGGCTAGTTCAGCTAGCTGGTACAGATAATTCAAAAGTCTGTTGGTTTTAATTTT
GTAACCTGTGGCCTGATCTGTAATAAACTTACATTTTTCAATAGGTAAAAA

FIGURE 108

CTGCAGGTAGACATCTCCACTGCCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT
GAAGGCCGGCCATACCAGAGTCCTGCCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG
TCTGTGCTGGTCTGAGGGTGCTGCCTGT**CATG**GGGGCAGCCATCTCCAGGGGGCCCTCATC
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGCTGCTGCTCTGGGTATCCTCTGCTG
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTCTGAATCCAGTCCCACTCCAGCCC
TGGCCCCTGTCCTGAGAAGGCCCCACCACCCAGAAAGCCAGCCATGAAGGCAGTACCTGC
TGCAGCCCTGAAGGCCCCCTGGCCTAGCCTGGAGCCAGGACC**TAA**GTCCACCTCACCTAGAG
CCTGGAATTAGGATCCCAGAGTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT
TGGAGCTGGACCCAGCGGCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC
TAAGGAGATGGGCCTGGGGTGGGGGCTTATGAGTTGGTGCTAGAGCCAGGGCCATCTGGACT
ATGCTCCATCCCAAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTTCCCTAGGCTGAGCACC
TCTAGGCCCTCTAGGTTGGGGAAGCAAACCTGGAACCCATGGCAATAATAGGAGGGTGTCCAG
GCTGGGCCCTCCCTGGTCCTCCCACTGTTTGCTGGATAATAAATGGAACATATGGCTCTAA
AAAAAAAAAAAAAAAAA

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FIGURE 109

MGAAISQGALIAIVCNGLVGFLLLLWVILCWACHSRLPTLTLSLNPVPTPALAPVLRPHH
PRSPAMKAATCCSPEGPWPSLEPRT

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FIGURE 110

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCA
 GTTCCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTA
 CTCCTTATTTGCATCTGTTTTGATAAATGATGTTGACACCCTCCACCGAATTCTAAGTGAA
 TC**CATG**TCGGGAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCC
 ATGATGTTTACCTTCAGATTCATCACCACCCTTCTGGTTCACATTTTCATTTTCATTGGTTAT
 TTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACC
 TCAGCATAGAATTGGACACAGAAAGGGAAAATATGAAGTGCCTGCTGGGGTTTGTATCGTA
 TCCACAGGCATCAGGCAGTGTCTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATT
 GACAGTTGAGCTTTTCCAAATCACAAATAAAGCCATCAGCAGTGTCTCCCTTCCTGCTGTTC
 AGCCACTGTGGACATTTGCCATCCTCATTTTCTTCTGGGTCTCTGGGTGGCTGTGTGCTG
 AGCCTGGGAACTGCAGGAGCTGCCCAGGTTATGGAAGCGGCCAAGTGGAATATAAGCCCCCT
 TTCGGGCATTTCGTACATGTGGTCGTACCATTTAATTGGCCTCATCTGGACTAGTGAATTCA
 TCCTTGCGTGCCAGCAAATGACTATAGCTGGGGCAGTGGTTACTTGTATTTC AACAGAAGT
 AAAAATGATCCTCCTGATCATCCATCCTTTCGTCTCTCTCCATTCTCTTCTTCTACCATCA
 AGGAACCGTTGTGAAAGGGTCATTTTTAATCTCTGTGGTGAGGATTCGAGAATCATTTGTCA
 TGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGTCCAGGTACCTGTTCCGA
 TGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA
 TACTACAAGTCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAATCT
 TGTCCAAGAACTCAAGTCACCTTTACATCTATTAAGTCTTTGGAGACTTCATAATTTTTCTA
 GGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTACAATCG
 GGCATTCCAGGTGTGGGCAGTCCCTCTGTTATGGTAGCTTTTTTTGGCTACTTAGTAGCCC
 ATAGTTTTTTATCTGTGTTTGAAGTGTGCTGGATGCACTTTTCTGTGTTTTGCTGTTGAT
 CTGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTT
 CGTAAAAAGGAGCAACAAATTAAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAGGA
 ATGAGGAGGGAACAGAACTCCAGGCCATTGTGAGAT**TAG**ATACCCATTTAGGTATCTGTACCT
 GGAAAAATTTCTTCTAAGAGCCATTACAGAATAGAAGATGAGACCACTAGAGAAAAGTT
 AGTGAAATTTTTTTTTAAAGACCTAATAAACCCCTATTCTTCTCTCAAAA

MSGRDITLGLCILALSLAMMFTFRFITTLVHFISLSVLGLLFCVCGVLWWLYDYDTNDL
SIELDTERENMKCVLGFIAIVSTGITAVLLVLIFVLRKRRIKLTVELFQITNKAISSAPFLLFQ
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI
LACQQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVM
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAVYTTTAINGTDFCTSAKDAFKIL
SKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAQVWAVPLLLVAFFAYLVAH
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN
EEGTLEQAIVR

FIGURE 112

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTTGGACCTCTCCCTGTTTCTTCCTT
 AGAATAATTTGTATGGGATTTGTGATGCAGGAAAGCCTAAGGGGAAAAAGAAATATTCATTCTG
 TGTGGTGAAAATTTTTTGAAAAAAAATTCCTTCTTCAAACAAGGGTGTCATTCTGATATT
TATGAGGACTGTTGTTCTCACTATGAAGGCATCTGTTATTGAAATGTTCCTTGTTTTGCTGG
 TGACTGGAGTACATTCAAACAAAGAAACGGCAAAGAAGATTAAAGGCCAAAGTTCACTGTG
 CCTCAGATCAACTGGCATGTCAAAGCCGGAAGATCATCGATCCTGAGTTTATTGTGAAATG
 TCCAGCAGGATGCCAAGACCCCAATACCATGTTTATGGCAGTACGCTGTATGATGCATCCTACT
 CCAGTGTGTGGGCGCTGCCGTACACAGTGGTGTGCTTGATAATTCAAGGAGGAAAAATACTT
 GTTCGGAAGGTTGCTGGACAGTCTGGTTACAAAGGGAGTTTATCCACGGTGTTCCAAATCGTT
 ATCCCTACCAGATGGAGAGAATCCTTTATCGTCTTAGAAAGTAAACCCAAAAAGGGTGTA
 CCTACCCATCAGCTCTTACATACTCATCATCGAAAAGTCCAGCTGCCAAGCAGGTGAGACC
 ACAAAGCCTATCAGAGGCCACTATTCAGGGACAACCTGCACAGCCGGTCACTCTGATGCA
 GCTTCTGGCTGTCACTGTAGCTGTGGCCACCCCCACCACCTTGCCAAGGCCATCCCCCTTCTG
 CTGCTTCTACACCAGCATCCCCAGACCACAATCAGTGGGCCACAGGAGCCAGGAGATGGAT
 CTCTGGTCCACTGCCACTTACACAGCAGCAAAACAGGCCAGAGCTGATCCAGGTATCCCA
 AAGGCAAGATCCTTCAGGAGCTGCCCTCCAGAAACCTGTTGGAGCCGATGTCAGCCTGGGAC
 TTGTTCCAAAAGAAATTTGAGCACACAGTCTTTGGAGCCAGTATCCCTGGAGATCCAAAC
 TGCAAAATTGACTTGTGTTTTTAATTGATGGGAGCACCAGGATTGGCAACGGCGATTCCG
 AATCCAGAAGCAGCTCCTGGCTGATGTTGCCCAAGCTCTTGACATTGGCCCTGCCCGTCCAC
 TGATGGGTGTTGTCCAGTATGGAGACAACCTGCTACTCACTTTAACTCAAGACACACAG
 AATTCTCGAGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGAGGACTTTCTAATGT
 AGGTGGGGCCATCTCCTTTGTGACCAAGAACTTCTTTCCAAAGCCATGGAACAGAGCG
 GGGCTCCCAATGTGGTGGTGGTGGTGGATGGCTGGCCACCGACAAGTGAGAGGAGCT
 TCAAGACTTGCAGAGAGATCAGGAATCAACATTTTCTTCATCACCATTGAAGGTGCTGCTGA
 AAATGAGAAGCAGTATGTGGTGGAGCCCACTTTGCAACAAGGCCGTGTGCAGAACAAACG
 GCTTCTACTCGCTCCACGTGCAGAGCTGGTTGGCCTCCACAAAGACCTGCAAGCCTTGGTG
 AAGCGGGTCTGCGACACTGACCGCCTGGCCTGCAGCAAGACCTGCTTGAACCTCGGCTGACAT
 TGGCTTCGTATCGACGGCTCCAGCAGTGTGGGACGGGCACTTCCGACCCGTCTCCAGT
 TTGTGACCAACCTCACCAGAGTTTGAGATTTCGACACGGACACGCGCATCGGGGCGGTG
 CAGTACACCTTACGAACAGCGGCTGGAGTTTGGGTTTGACAAGTACAGCAGCAAGCCTGACAT
 CCTCAACGCCATCAAGAGGGTGGGCTACTGGAGTGGTGGCACAAGCAGCGGGGCTGCCATCA
 ACTTCGCCCTGGAGCAGCTCTTCAAGAACTCAAGCCCAACAAGAGAGTTAATGATCCTC
 ATCACCGACGGGAGGTCTACGACGACGTCCGGATCCAGGCATGGCTGCCCATCTGAAGGG
 AGTGATCACCTATGCGATAGCGGTTGCCTGGGCTGCCAAGAGGAGCTAGAAGTCAATTGCCA
 CTCACCCCGCCAGAGACCCTCCTTCTTTGTGGACGAGTTTGACAACCTCCATCAGTATGTC
 CCCAGGATCATCCAGAACATTTGTACAGAGTTCAACTCACAGCCTCGGAACTGAATTTCAGAG
 CAGGCAGAGCACCAGCAAGTGTGCTTTACTAACTGACGTGTTGGACCACCCACCGCTTAA
 TGGGCGCAGCGACGGTGATCAAGTCTTGGGCAGGGCATGGAGAAACAATGTCTGTTATTA
 TTCTTTGCCATCATGCTTTTTCATATTCAAAACCTTGAGTTTACAAAGATGATCACAAACGT
 ATAGAATGAGCCAAAAGGCTACATCATGTTGAGGGTGTGGAGATTTTACATTTTGACAAAT
 GTTGAGATTTTTAAGTTGTTATTTCTGATTTGAACCTCTGTAACCCCTCAGCAAGTTTCATTTT
 GTCATGACAAATGTAGGAATGCTGAATTAATGTTTAGAAGGATGAAAAATAAAAAAAAAA
 AA
 AA

FIGURE 113

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKC
PAGCQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSL
SLPRWRESFIVLESKPKKGVTYPSALTYSSSKSPAAQAGETTKAYQRPPPIPGTTAQPVTLMQ
LLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSEQEMDLWSTATYTSSQNRPRADPGIQ
RQDPGGAFFQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRFR
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNSRDLKTAIEKITQRGGLSNV
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAE
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTLPVKRVCDTDRLACSKTCLNSADI
GFVIDGSSSVGTGNFRTVLQFVTNLKFEFEISDTRIGAVQYTYEQRLEFGFDKYSSKPD
LNAIKRVGYWGGTSTGAAINFALQLFKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKG
VITYAIGVAWAAQEELEVIATHPARHSSFVDEFNLHQYVPRIIQNICTEFNSQPRN

FIGURE 114

CAGGATGAACTGGTTGCAGTGGCTGCTGCTGCTGCGGGGCGCTGAGAGGACACGAGCTCTA
TGCCTTTCCGGCTGCTCATCCCGCTCGGCCTCCTGTGCGCGCTGCTGCCCTCAGCACCATGGT
 GCGCCAGGTCCCCACGGCTCCGCGCCAGATCCCGCCACTACAGTTTTTCTCTGACTCTAAT
 TGATGCACTGGACACCTTGCTGATTTTGGGAATGTCTCAGAATCCAAAGAGTGGTTGAAG
 TGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCTCTGTGTTTGAACAAACATT
 CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGAAGTAGA
 GGCTGGATGGCCCTGTTCCGGGCTCTCCTGAGAAATGGCTGAGGAGGCGGCCGAAAACCTCC
 TCCAGCCTTTCAGACCCCCACTGGCATGCCATATGGAACAGTGAACCTACTTCATGGCGTG
 AACCCAGGAGAGACCCCTGTACCTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC
 CACCTTGAGCAGCCTCACTGGTGACCCGGTGTTTGAAGATGTGGCCAGAGTGGCTTTGATGC
 GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCGGCAACCACATTGATGTGCTCACTGGC
 AAGTGGGTGGCCAGGACGCAAGCATCGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGT
 GAAAGGAGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCTTAGAGTATAACAAAG
 CCATCCGGAACCTACACCCGCTTCGATGACTGGTACCTGTGGGTTTCAGATGTACAAGGGGACT
 GTGTCCATGCCAGTCTTCCAGTCCTTGGAGGCCTACTGGCCTGGTCTTCAGAGCCTCATTGG
 AGACATTGACAAATGCCATGAGGACCTTCTCAACTACTACACTGTATGGAAGCAGTTTGGGG
 GGCTCCCGGAATTCTACAACATTCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTACCCA
 CTTTCGGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCCACCCT
 CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAATCAGCAAGGTGGAGTGC GGAT
 TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCGTTCTTCCTG
 GCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCAACCAACTTCATCCACAACATGG
 GTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGCATCCTGGGGGCTGGGGGTACAA
 TCTTCAACACAGAAGCTCACCCATCGACCTTGCCGCGCTGCACTGTGCCAGAGGCTGAAG
 GAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATCTACTCTCTCAAACGGAGCAGGTC
 GAAATTTAGAAAAACACTGTAGTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACAC
 TCTTCTCACCAGAAAACCATGACCAGGCAAGGGAGAGGAAGCCTGCCAAACAGAAGGTCCCA
 CTTCTCAGCTGCCCCAGTCAGCCCTTCACCTCCAAGTTGGCATTACTGGGACAGGTTTTCTT
 AGACTCCTCATTAACCACTGGATAATTTTTTTATTTTTTTATTTTTTTGAGGCTAAACTATAATA
 AATTGCTTTTGGCTATCATAAAA

MPFRLLIPLGLLCALLPQHHPAGPDGAPDPAHYSFSLTLIDALDTLLILGNVSEFQRVVE
VLQDSVDFDIDVNASVFETNIRVVGGLLSAHLSSKKAGVEVEAGWPCSGPLLRMAEEAARKL
LPAFQTPTGMPYGTVNLHGVNPGETPVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALM
RLWESRSDIGLVGNHIDVLTGKWAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK
AIRNYTRFDDWYLVWQMYKGTVSMVPVQSLSEAYWPLQSLIGDIDNAMRTFLNYYTVWKQFG
GLPEFYNI PQGYTVEKREGYPLRPELIESAMYLYRATGDP T LLELGRDAVESIEKISKVECG
FATIKDLRDHKL DNRMESFFLAETVKYLYLLFDP T NFIHNGSTFDVAITPYGECILGAGGY
IFNTEAHPIDLAALHCCQRLKEEQWEVDLMREFYSYLSKRSRKFQKNTVSSGWPWEPPARPGT
LFSPENHDQARERKPAKQKVPLLSCPSPQFTSKLALLGQVFLDSS

1000 1000 1000 1000 1000 1000 1000 1000 1000 1000

AAGATTACATTTTCTTGGAACTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTG
 GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCCGCTCTAGAACA
 ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
 GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA
AATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
 ACGCATTGATTCCATGTTTGCTCAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC
 TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCAGTGATCGCGCCTGGAGA
 AACAGTGTACTATTCTGTGGAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
 GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTGATGTCAGTGATGACATC
 ACGGCCACTGTGCCATACAACCTTCGTGTCAAGGCCACATTGGGCTCAGACCTCAGCCTG
 GAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTACCCGACCTGGGATGGAGA
 TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC
 CTGTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG
 GGGTATTCCAGTGCACTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCAGA
 CATTCGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
 GGAGAGGCCATTCCCTTGGTACTGGCCCTGTTTGCCCTTTGTGTGGCTTCATGCTGATCCTTGT
 GGTGCTGCCACTGTTTGTCTGGAATAATGGGCCGCTGCTCCAGTACTCCTGTTGCCCGTGG
 TGGTCTCTCCAGACACCTTGAAATAACCAATTACCCCCAGAAGTTAATCAGCTGCAGAAGG
 GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACCTCCTCAGGGCCTGGAT
 CTCAT**AGG**GTTTGCGGAAGGGCCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAC
 ATGAGGGGACAAGTTGTGTTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
 GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGTTTTGTCTAACAGAACAC
 TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGCTGCCACTTGCTGGCTGAGCAAC
 CTGGGAAAAGTGACTTCATCCCTTCGGTCTAAGTTTTCTCATCTGTAATGGGGGAATTACC
 TACACACCTGCTAAACACACACACAGAGTCTCTCTATATATACACAGTACACATAAA
 TACACCCAGCACTTGCAAGGCTAGAGGGAAACTGGTGACACTCTACAGTCTGACTGATTGAG
 TGTTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
 GGCTTGAGAGAGCCACTTCCAGAAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
 TGTGAGTTCACTTCAAGCCCAATGCCGCTGAGAGGGGAATGGCTTAGCGAGCTCTACAGT
 AGGTGACCTGGAGGAAGGTACAGCCACACTGAAAATGGGATGTGCATGAACACGGAGGATC
 CATGAACTACTGTAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT
 GTGCAATGCGACGAGAATGAGAAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTC
 GTTGGTAAAGTACAGAATTACAGCAAATAAAAAGGGCCACCTGGCCAAAAGCGGTAAAAA
 AAAAAAAAAA

FIGURE 117

MQTFTMVLEEIIWTSIFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLWSPVIAPGE
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITATVPYNLRVRATLGSQTS
SILKHPFNRNSTILTRPGMEITKDGPHLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPVLVLFVAFVGFMLILV
VVPLFVWKMGRLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation sites.

amino acids 40-43 and 134-137

Tissue factor proteins homology.

amino acids 92-119

Integrins alpha chain protein homology.

amino acids 232-262

FIGURE 118

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTGCAATACCAGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG
ATGTCACTGATGACATCACGGCCACTGTGCCATAACAACCTTTGTGTCAAGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCCTTGTTGGCCTANTGGAGGAGGGGCGAACCCCTTGCGGCGCAAGGG
GTTNGCGAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCCAC
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

FIGURE 119

CGGACGCGTGGGCGGCCACCTCCGGAACAAGCC**ATG**TGGCGGCGACGGTGGCAGCGGCGTG
GCTGCTCCTGTGGGCTGCGGCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGG
TCAACATCCGGGGCAAACCTGGTGTGCTGGAGAAGTACCGGGATCGGTGTCCCTGGTGGTG
AATGTGGCCAGCGAGTGCGGCTTACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG
AGACCTGGGCCCCACCACTTTAACGTGCTCGCCTTCCCCTGCAACCAGTTTGGCCAAACAGG
AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCCGCCGACCTACAGTGTCTCATTTCCC
ATGTTTAGCAAGATTGCAGTCACCGGTACTGGTGCCATCCTGCCTTCAAGTACCTGGCCCA
GACTTCTGGGAAGGAGCCCCACCTGGAACCTTCTGGAAGTACCTAGTAGCCCCAGATGGAAAG
TGGTAGGGGCTTGGGACCCAACCTGTGTCACTGGAGGAGGTGAGACCCAGATCACAGCGCTC
GTGAGGAAGCTCATCCTACTGAAGCGAGAAGACTTA**TAA**CCACCGCGTCTCCTCCTCCACCA
CCTCATCCCGCCCACCTGTGTGGGCTGACCAATGCAAACCTCAAATGGTGTCTCAAAGGGAG
AGACCCACTGACTCTCCTTCCTTTACTCTTATGCCATTGGTCCCATCATTCTTGTGGGGGAA
AAATTCTAGTATTTTGATTATTTGAATCTTACAGCAACAAATAGGAACTCCTGGCCAATGAG
AGCTCTTGACCACTGAATCACCAGCCGATACGAACGTCTTGCCAACAAAATGTGTGGCAA
TAGAAGTATATCAAGCAATAATCTCCACCCAAGGCTTCTGTAAACTGGGACCAATGATTAC
CTCATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC
CAAATAGGAGGCATTCAATGAACATTTTTTGCATATAAACCAAAAAATAACTTGTTATCAAT
AAAAACTTGCATCCAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTT
GTTATTTCTCTGTATTATTTTCTTCATTACAAAAGAAATGCAAGTTCATTGTAACAATCCA
ACAATACCTCACGATATAAAAATAAAAATGAAAGTATCCTCCTCAAAAA

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FIGURE 120

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLVKYRGSVSLVVNVASECGFTDQ
HYRALQQLQRDLGPHHFNVLAFFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG
AHPAFKYLAQTSKGKEPTWNFWKYLVPDGVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

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CGGACGCGTGGGCGGGCCGGGACGACAGGGAACAGCGAGCCATGGCTGTCTACGTCGGGATGTGGCGCTGGGAGGCTGTGGCCGGGAGCTCGGGGGTCTGGGGGCGGGGCGCCCTCTCTCGGATTTGGCAGGAAGTCAGGTTGTCAGGTTGTCGCTTCTCAGTCCAGAGAGTGGATCGCATGGTCTCCACGCCCATCGGAGGCCTCAGCTACGTTTCAAGGGTGACCAAAAAGCATCTTACACGCAAGACTGTGGGCCAGTGCTCGGAGACCAACAGCAGAGGTCACAGAGCAGAGGCCCTTGGTGCTCTCCATGAAGACCTCAGTTGACCTTTGCCAACTCAAGGAGAGGTGGACAAAGTGTCTTGGCTTGGCCCTCGTGACATTGGCCCTGCAAAAGGTGACCGGCTGGGCATGTGGGGACTAACTCTCTATGGGTGCTCATGCACTTGGCCACCGCCAGCGGCATCATCTCGTGCTGTGAACCCGACCTACCGACTATGGAAGTATGGAGTGTCTCTCAAGAAGTGGGCTGCAAGGCCCTTGTGTCCCCAAGCAATTCAAGACCAGCAATACTACACGCTCGAAGCAGATCTGTCCAGAAGTGGAGAATGCCCAGCCAGGGGCTTGAAGAGTCAGAGGCTCCAGATCTGACCAACGTCATCTGGTGGATGCCCTTGGCGGGACCTGCTCTGGATGAAGTGGTGGCGGTGGCAGCACGCGGAGCATCTGGACCAGTCCAATAACCAAGCAGATTCTGTCTGCCGATACCCCATCAACATCCAGTTCACCTCGGGGACAACAGGCAGCCCCAAGGGGGCCACCCTCTCCACATACAACATGTCAACACATCCAACTTTAGAGAGAGCGCTGAAACTGCATGAGAAGACACAGAGCAGTTGGCGGATGATCTCTGCCAACCCCTGTACCAATTGCGCTGGGTTCCGTGGCAGGACCAATGATGTGCTGATGTACGTTGCCACCCCTCATCTGGCCTCTCCCATCTTCAATGGCAAGAAGCAGCTGGAGGCCATCAGAGAGAGAGAGGACCTTCTCGTATGGTACCCCAAGATGTTCTGTGGACATTCTGAACCAAGCCAGACTTCCAGATTATGACATCTGACCATGTGTGGAGGTGTATTGCTGGGTTCCCTGCACTCCAGAGTTGATCCGAGCCATCATCAACAGATAAATATGAAGGACCTGGTGGTTGCTTATGGAACCAAGAGAGAACGTCCTGTGACATTGCGGCACTTCCCTGAGGACCTGGGAGCAGAGGCAAGGACGTGGGCAGAAATTGCTCTCACAGCGAGGCCGATCATGAACATGGAGGACGAGCGCTGGCAAAGCTGAACAGCCCGGGGAGCTGTGCTCGAGGGTACTGCGTCATGCTGGGCTACTGGGCTGAGCTCGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGTATTTGGACAGGATGTGCGCCATGAATGAGCAGGGTCTGTGAGATCGTGGGCGCTCTAAGGATTGATCATCCGGGTTGTGAGAATCTACCCCGAGAGCTCGAGGACTCTTTTACACACACCCGAAGGTGCAGGAAGTGCAGGTGGTGGGAGTGAAGGACGATCGGATGGGGGAAGATTTTGGCTCTCGGCTGAAGGACGGGGAGGAGACCAGGTGGAGGAGATAAAGCTTTGCAAAAGGGAAGATCTCTCACTCAAGATTCCGAAGTACATGTGTTTGTCCAAAACCTACCCCTCACCATTTTCAAGAAAGATCCAGAAATCAAACCTTCGAGACAGATGGAACGCATCTAAATCTCTCAATTAAGCAGCAGGCGTGTCTTGGCCGTTGGCTTACTCTCTCTGCAGATGCAACCTGGCTTTATGCACTAGATCTCCCGACACCCAGTTTGTAGCCAGGCACATCAAAATGTGAGCCAGGCACATCAAAATGTCAAGAAATGTGACTGAACGAACTAAGAGCTCTCGGATGGGTCGGGAATCGCTGGGCGCAAGGTGCCAAAGGCAGGCAGCCTGCCAGGCGCTCCCTCTGTCCATCCCAACATCCCTCTGTCTGTCTTGTGATTGGCATTAAGAGCTTCTGTTTTCTTTGAAAAA

FIGURE 122

MAVYVGLRLRLGRLCAGSSGVLGARAALSRWQEARLQGVRFSSREVDRMVSTPIGGLSYVQ
GCTKKHLNSKTVGQCLETTAQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG
DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVFPKQFKTQQY
YNVLKQICPEVENAQPGALKSQRLPDLTTVISVDAPLPGTLLLDDEVVAAGSTRQHLDQLQYN
QQFLSCHDPINIQFTSGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY
HCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY
DISTMCGVIAGSPAPPELIRAIINKINMKDLVVAYGTTENS PVTFAHFPEDTVEQKAESVG
RIMPHTEARIMNMEAGTLAKLNTPGELCIRGYCVMLGYWGEPOKTEEAVDQDKWYWTGDVAT
MNEQGFCIKIVGRSKDMIIRGGENIYPAELEDFHTHPKVQEVQVVGKDDRMGEEICACIRL
KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL

Signal Peptide:

amino acids 1-22

Transmembrane Domains:

amino acids 140-161, 213-229, 312-334

Putative AMP-binding Domain Signature:

amino acids 260-271

N-myristoylation Sites:amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
314-319, 318-323, 379-384, 380-385, 409-413**N-glycosylation Site:**

amino acids 282-285

FIGURE 123

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA
TGATCCTGCCCAACCCCTGTACCATTGCCTGGGTCCGTGGCAGGCACAATGATGTGTCTG
ATGTACGGTGCCACCCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACCTGGAGGC
CATCAGCAGAGAGAGAGGCACCTTCCTGTATGGTACCCCCACGATGTTCTGTGGACATTCTGA
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAATATGAAGGACCTGGTGGT
TGCTTATGGAACCACAGAGAACAGTCCCGTGACATTCGCGCACTTCCCTGAGGACACTGTGG
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGCATCCGAGGGTACTGCGT
CATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT
ATTGGACAGGAGATGTCGCCAC

FIGURE 124

GAGCAGGACGGAGCCATGGACCCCGCCAGGAAAGCAGGTGCCAGGCCATGATCTGGACTGC
 AGGCTGGCTGCTGCTGCTGCTGCTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG
 TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAAGTGC GCGCGCCGGG
 GTGGACGTCTGCACCGAGGCCGTGGGGCGGTGGAGACCATCCACGGAACAATTCTCGCTGGC
 AGTGCGGGGTTCGGGTTTCGGGACTCCCCGGCAAGAATGACCGCGGCCTGGATCTTCACGGGC
 TTCTGGCGTTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTC
 ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGATACCCGCCAACGGCGTGGAGTG
 CTACAGCTGTGTGGGCCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCCGGTTCGTGAGCT
 GCTACAACGCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTACCTTGACGGCA
 GCTAATGTGACTGTGTCTTGCCTGTCCGGGGCTGTGTCCAGGATGAATTCTGCACTCGGGA
 TGGAGTAACAGGCCAGGGTTCACGCTCAGTGGCTCCTGTTGCCAGGGGTCCCGCTGTAAC
 CTGACCTCCGCAACAAGACCTACTTCTCCCTCGAATCCACCCCTTGTCGGGTGCCCCCT
 CCAGAGCCACGACTGTGGCCTCAACCACATCTGTACCACCTTCTACCTCGCCCCAGTGAG
 ACCCACATCCACCACCAAAACCCATGCCAGCGCCAACCAAGTCAGACTCCGAGACAGGGAGTAG
 AACACGAGGCCTCCCGGGATGAGGAGCCAGGTTGACTGGAGGCGCCGTGGCCACCAGGAC
 CGCAGCAATTCAGGGCAGTATCCTGCAAAAGGGGGCCCCAGCAGCCCCATAATAAAGGCTG
 TGTGGCTCCACAGCTGGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTACTGTT
GAGCTTCTCCACCTGGAAATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCT
 CATCACTTCTGTTCCACCACTGGACTGGGCTGGCCAGCCCCGTGTTTTTCCAACATTCCC
 CAGTATCCCCAGCTTCTGTGCGCTGGTTTTCGGGCTTTGGGAAATAAAATACCGTTGTATAT
 ATTCTGCCAGGGGTGTTCTAGCTTTTTTGAGACAGCTCCTGTATCCTTCTCATCCTTGCTCTC
 TCCGCTTGCTCTTGTGATGTTAGGACAGAGTGAGAGAAGTCAGCTGTACGGGGAAGGTG
 AGAGAGAGGATGCTAAGCTTCTACTCACTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGG
 GGTGGGTGGGACAATGGCTCCCCACTCTAAGCACTGCCTCCCTACTCCCCGCATCTTTGGG
 GAATCGGTTCCTCATATGTCTTCTTACTAGACTGTGAGCTCCTCGAGGGGGGGCCCCGTAC
 CCAATTGCCCCATATAGTGAGTCGTA

MDPARKAGAQAMIWTAGWLLLLLLRGGAALECYSCVQKADDDGCSPNKMKTVKCAPGVDVCT
EAVGAVETIHGQFSLAVRGCGLPGKNDRGLDLHGLLAFIQLQQCAQDRCNAKNLNLSRAL
DPAGNESAYPPNGVECYSCVGLSREACQGTSPVVSVCYNASDHVYKGCDFGNVLTAAANVTV
SLPVRGCVQDEFCTRDGVTGPGFTLSGCCQGSRCNSDLRNKTYFSRIPPLVRLPPPEPTT
VASTTSVTTSTSAVRPTSTTKMPAPTSTQTPRQGEHEASRDEEPRLTGGAAGHQDRNSNG
QYPAKGGPQQPHNKGCVAPTAGLAALLAVAAGVLL

FIGURE 126

[illegible]

FIGURE 127

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLILSRCK
CSFNQKPRAPGDEEAQVENLITANATEPQKQRTVEQPSGGSLWNLRRLLEPLDANVDA

[illegible]

FIGURE 128

AAACTTGACGCCATGAAAGATCCCGGTCCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT
CCTCTGCCCCAGGGAGCCACCCTGGGTGGTCCTGAGGAAGAAAGCACCATTGAGAATTATG
CGTCACGACCCGAGGCCCTTTAACACCCCGTTCCTGAACATCGACAAATTGCGATCTGCGTTT
AAGGCTGATGAGTTCCTGAACTGGCAGCCCTCTTTGAGTCTATCAAAGGAAACTTCCTTT
CCTCAACTGGGATGCCTTTCCCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCCAGT
GACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT
CTTCCTGCCTCAGGAACTCCAATAAAACATTTTCCATCCAAA

CCCTTCCTGCCTCAGGAACTCCAATAAAACATTTTCCATCCAAA

FIGURE 129

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

FIGURE 131

MGVEIAFASVILTCLSLAAGVSQVLLQPVPTQETGPKAMGDLSCGFAGHS

FIGURE 132

GGGGAATCTGCAGTAGGTCTGCCGGCG**ATGG**AGTGGTGGGCTAGCTCGCCGCTTCGGCTCTG
 GCTGCTGTTGTTCTCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAAATGGA
 AAGTATTTATTGACCAAATTAACAGGTCCTTTGGAGAATTACGAACCATGTTCAAGTCAAAAC
 TGCAGCTGCTACCATGGTGTCTAGAGAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAG
 GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACA
 GACTGTACCGGAAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATT
 TTGGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCA
 GGTTCCTAAATGGATGGAGCCTGCCATCCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC
 ATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGGACCTGCTGTTTGGCCAAATTTAT
 CCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTGAGCAGCACAGTG
 GCCATGGA AAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAG
 ATCCTCTCATTCTTCTGTCTCGGAAAAACCCAAAACCTTGTGATGCGAATACACCAAAAC
 CAGGCCTGGAATCTATGAAGATACTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGT
 GGATCACTGCAAATACAAGTATCTGTTTAAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTA
 AACACCTCTTCTGTGTGGCTCACCTGTTTCCATGTTGGTGATGAGTGGCTAGAATCTTCT
 TATCCACAGCTGAAGCCATGGGTTCACTATATCCAGTCAAAACAGATCTCTCCAATGTCCA
 AGAGCTGTTACAATTTGTAAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAA
 GCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCCTTTG
 AGTGAATACTCTAAATTCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTAT
 TCCCAAAATGTTGAAAACCTGAACTA**TAG**TAGTCATCATAGGACCATAGTCCTCTTTGTGGCA
 ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA
 TCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGCTGCACCCAGAGCAACTCTTGAGA
 AAGATTTAAATGTGTCTAATACACTGATATGAAGCAGTTCAACTTTTTTGGATGAATAAGGA
 CCAGAAATCGTGAGATGTGGATTTTGAACCCAACTCTACCTTTCATTTTCTTAAAGCCAATC
 ACAGCTTGTGCCCTCAGATCATCCACCTGTGTGAGTCCATCACGTGAAATTGACTGTGTCCA
 TGTGATGATGCCCTTTGTCCCATTATTTGGAGCAGAAAATTCGTGATTTGGAAGTAGTACAA
 CTCATTGCTGGAATTGTGAAATTATTCAGGCGTGATCTCTGTCACTTTATTTTAAATGTAGG
 AAACCTATGGGGTTTATGAAAAATACTTGGGGATCATTCTCTGAATGGTCTAAGGAAGCGG
 TAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTGTAAAACCATAAACTCTGTTACTCAG
 GAGGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATTGCAATTGGATT
 TCAGGTTCCCTTTTTGTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

FIGURE 133

MEWWASSPLRLWLLLFLLPSAQGRQKESGSKWKVFDQINRSLENYEPCSSQNCSCYHGVIE
EDLTPFRGGISRKMMAEVVRRKLGTHYQITKNRLYRENDCMFPSRCSGVEHFILEVIGRLPD
MEMVINVRDYPQVPKWMEPAIPVFSFSKTSEYHDIMYPAWTFWEGGPAVWPIYPTGLGRWDL
FREDLVRSAAQWPWKKKNSTAYFRGSRTPERDPLILLSRKNPKLVDAEYTKNQAWKSMKDT
LGKPAAKDVHLVDHCKYKYLNFNFRGVAASFRFKHLFLCGSLVFHVGDWLEFFYPQLKPWVH
YIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQMDDITCYWENLLSEYSKFLSY
NVTRRKGVDQIIPKMLKTEL

133-405664

FIGURE 134

CACCCCTCCATTTCTCGCCATGGGCCCTGCACTGCTCCTGATCCCTGCTGCCCTCGCCTCTT
 TCATCCTGGCCTTTTGGCACCCGGAGTGGAGTTTCGTGCGCTTTACCTCCCTTCGGCCACTTCTT
 GGAGGGATCCCGGAGTCTGGTGGTCCGGATGCCCCGCCAGGGATGGCTGGCTGCCCTGCAGGA
 CCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTTGTTGGGCAGC
 ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCCCTCAG
 AGGTCACTGTATGTGGCCTGCACTGCCCTGGCCTTGCAGCTGGTGTATGCGGTACTGGGAGCC
 CATACCCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCGC
 TCCTCTGCTTTGTGCTCCATGTCATCTCCTGGCTCCTCATCTTTAGCATCCTTCTCGTCTTT
 GACTATGCTGAGCTCATGGGCCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCGAGCC
 TCTGGCCCTGAAGTCTCCCCGGGCTCTCAGACTCTTCTCCACCTGCGCCACCCAGTGTGTG
 TGGAGCTGCTGACAGTGTGTGGGTGGTGCTACCTGGGCACGGACCGTCTCCTCCTTGCT
 TTCTCCTTACCCTCTACCTGGGCTGGCTCACGGGCTTGATCAGCAAGACCTCCGTACCT
 CCGGGCCAGCTACAAAGAAAACCTCCACCTGCTCTCTCGGCCCCAGGATGGGGAGGCAGAGT
GAGGAGCTCACTCTGGTTACAAGCCCTGTTCTTCTCTCCCACTGAATTCTAAATCCTTAAC
 ATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCCAAATCCATGGACTGAAGGAGATGCCCCTT
 CTACTACTTGAGACTTTTATTCTCTGGGTCCAGCTCCATACCCTAAATTCTGAGTTTCAGCCA
 CTGAACTCCAAGGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC
 TTCACTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCTGCC
 CTGACCACTCCCCTGGCACTGTTAATTGCCTCTGCGCCTCAGGGGTCCCCTTCTGCACCGCT
 GGCTTCCACTCCAAGAAGGTGGACCAGGGTCTGCAAGTTCAACGGTCATAGCTGTCCCTCCA
 GGCCCCAACCTTGCTCACCACCTCCCGGCCCTAGTCTCTGCACCTCCTTAGGCCCTGCCTCT
 GGGCTCAGACCCCAACCTAGTCAAGGGGATTCTCCTGCTCTTAAGTGCATGACTTGGGGCTC
 CCTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAATAAAGTCAGCCTTTTTCTAAAAAAA

FIGURE 135

MAPALLLIPAAALASFILAFGTGVEFVRFSTSLRPLLGGIPESGGPDARQGWLAALQDRSILAP
LAWDLGLLLLLFVGQHSMAAERVKAWTSRYFGVLQRSLYVACTALALQLVMRYWEPIPKGPV
LWEARAEPWATWVPELLCFVLHVISWLLIFSILLVFDYAELMGLKQVYYHVLGLGEPLALKSP
RALRLFSHLRHPVCVELLTVLWVPTLGTDRLLLAFLLTLYLGLAHGLDQQDLRYLRAQLQR
KLHLLSRPQDGEAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

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FIGURE 137

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQD
FHFTLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEA EK
EDKMLALSLEDEHLLYGDIIHQDFLDTYNNLT LKTIMAFRWVTEFCPNAKYVMKTD TDVFIN
TGNLVKYLNLNLHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPYCSGLGYIMSRD
LVPRIYEMMGHV KPIKFEDVYVGICLNLLKVNIHIPEDTNLFFLYRIHLDVCQLRRVIAAHG
FSSKEIITFWQVMLRNTTCHY

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FIGURE 140

CATTTCTGAAACTAATCGTGTCAGAATTGACTTTGAAAAGCATTGCTTTTTACAGAAGTATA
 TTAACTTTTTAGGAGTAATTTCTAGTTTGGATTGTAATATGAAATAATTTAAAGGGCTTCG
 CTCATATATAGGAAAATCGCATATGGTCCTAGTATTAAATCTTATTGCTTACTGATTTTTT
 TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAA
 GAATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTTTACATG
 CAAGCTTATAGTTGAAATATTTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGT
 TTGTTTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT
 CAGATTCGGTTGCCAACTCGTCCCCATTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAAT
 CCAGGAAATCTGCATAGAAAACCTTAGGCCTTTATACCAGAAAAAGCCAACTATGAATTAC
 TGGAAAAAGAAGTAGAAAAAAGAAAAGTAGCCTTACAAGAAGCCAAATTTAAAGCAAAGGGA
 TTGAATCCGATGGAACCTCCAGCCCTTTCAACCCTGGGTGGATTTTCTCCAGCCTCCAAGCC
 ATCATCACCAGAGAAGTAAAGCTGAAGAGAAATCACCAATCTCCATTAATGTGAAGACAG
 TCAAAAAGAACCTGAGGATAGACAACAGGCTTCCAAAAGCCCTTACAATGGTGTAAAGAAA
 GACAGCAAGAGAAGTAGAAATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGATCACG
 TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA
 GCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAAGCCCTCGAAGACATCATAATCAT
 GGTCTCCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAAACAGACATGG
 TCATAAAAGGAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG
 CCAAGAAACACAGGCATGAAAGGGGACATCATAGGACAGGCGTGAACGATCTCGCTCCTTT
 GAGAGGTCCCATAAAGCAAGCACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG
CTGACTTTCTCTTCTTTGAGCCTGCATCAGTTCTTGGTTTTGCCTATCTACAGTGTGATGT
 ATGGACTCAATCAAAAACATTAACGCAAACCTGATTAGGATTTGATTTCTTGAAACCCTCTA
 GGTCTCTAGAACACTGAGGACAGTTTCTTTTGAAAAGAACTATGTTAATTTTTTTGCACATT
 AAAATGCCCTAGCAGTATCTAATTA AAAACCATGGTCAGGTTCAATTGTACTTTATTATAGT
 TGTGTATTGTTTATTGCTATAAGAACTGGAGCGTGAATTCTGTAAAAATGTATCTTATTTTT
 ATACAGATAAAATTGCAGACACTGTTCTATTTAAGTGGTTATTGTTTAAATGATGGTGAAT
 ACTTTCTTAACACTGGTTTGTCTGCATGTGTAAAGATTTTACAAGGAAATAAAATACAAAT
 CTTGTTTTTTCTAAAAAAGG

FIGURE 141

MNDSLRTNVFVRFPETIACACIYLAARALQIPLPTRPHWFLFLFGTTEEEIQEICIETLRLY
TRKKPNYELLEKEVEKRRKVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEK
SPISINVKTVKKEPEDRQQASKSPYNGVRKDSKRSRNSRSASRSRSTRSRSRSHTPRRHYN
NRRSRSGTYSSRSRSHSESPRRHHNHGSPHLKAKHTRDDLKSSNRHGHKRRKSRSRSQ
SKSRDHSDAAKKHRHERGHHRDRRERSRSFERSHKSKHHGGSRSRSGHGRHR

[illegible][illegible]

FIGURE 143

GGCACGAGGCCTCGTGCCAAGCTTGGCACGAGGGTGACCCGCTTCTCGCACGCGTCA**ATGGC**
GGTCCCTCGGAGTACAGCTGGTGGTGACCCCTGCTCACTGCCACCCTCATGCACAGGCTGGCGC
CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTTTGTTCGGATACAAGCACCCG
TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGGAAAGAGCGGTG
GGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCCGAGATGCCCCGTTCCAGCTGG
AGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTGCGCTTCTTCTGGAGTACCACTGG
TTTGTGGACTTTGCTGTGTACTCGGGCGCGGTGTACCTCTTCACAGAGGCCCTACTACTACAT
GCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTCTTCTGGTGCCTGCTCACGGTGACCTTCT
CCATCAAGATGTTCTTGACAGTGACACGGCTGTACTTCAGCGCCGAGGAGGGGGGTGAGCGC
TCTGTCTGCCTCACCTTTGCGCTTCTCTTCTGCTGCTGGCCATGCTGGTGCAAGTGGTGCG
GGAGGAGACCCCTCGAGCTGGGCTGGAGCCTGGTCTGGCCAGCATGACCCAGAACTTAGAGC
CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCTGTGGCCAAGCTGGCTATCCGCGTG
GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCCTTCTCACCTTCCCAGGCCTGCGGCTGGC
CCAGACCCACCGGGAGCGCACTGACCATGTGCGAGGACAGACCCATGCTGCAGTTCCTCCTGC
ACACCAGCTTCTGTCTCCCTGTTTCATCCTGTGGCTCTGGACAAAGCCCATTGCACGGGAC
TTCCTGCACACGCGCCGTTTGGGGAGACGCGTTTCTCCCTGCTGTCCGATTCTGCCTTCGA
CTCTGGGCGCCTCTGGTTGCTGGTGGTGTGTGCCTGCTGCGGCTGGCGGTGACCCGGCCCC
ACCTGCAGGCCTACCTGTGCCTGGCCAAGGCCCGGTGGAGCAGCTGCGAAGGGAGGCTGGC
CGCATCGAAGCCCGTAAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT
GAGCTTGCAGTACCTGACGCCGCTCATCCTCACCTCAACTGCACACTTCTGCTCAAGACGC
TGGGAGGCTATTCTGGGGCTGGGCCAGCTCCTCTACTATCCCCGACCCATCCTCAGCC
AGCGCTGCCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCAGCGCGGATTGCCGG
GGCCCTGGGTGGCTGCTTACTCCCTCTTCTCCTCGTGCGCTCCTGGCCTACCTCATCTGGT
GGACGGCTGCCTGCCAGCTGCTCGCCAGCCTTTTCGGCCTCTACTTCCACAGCACTTGGCA
GGCTCCT**TAGC**TGCCTGCAGACCCTCCTGGGGCCCTGAGGTCTGTTCTGGGGCAGCGGGACA
CTAGCCTGCCCCCTCTGTTTGCGCCCCCGTGTCCCAGCTGCAAGGTGGGGCCGGACTCCCC
GGCGTTCCTTTCACACAGTGCCTGACCCGCGGCCCCCTTGGACGCCGAGTTTCTGCCTCA
GAACTGTCTCTCCTGGGCCAGCAGCATGAGGGTCCCAGGCCATTGTCTCCGAAGCGTATG
TGCCAGGTTTGTAGTGGCGAGGGTGATGCTGGCTGCTCTTCTGAACAAATAAGGAGCATGCC
GATTTTAA

MAVLGVQLVVTLLTATLMLHRLAPHCSFARWLLCNGSLFRYKHPSEELRALAGKPRPRGRKE
RWANGLSEEKPLSVPRDAPFQLETCPLTTVDALVLRFFLEYQWFVDFAVYSGGVYLFTEAYY
YMLGPAKETNIAVFWCLLTVTFSIKMFLTVTRLYFSAEEGERSVCLTFAFLFLLLAMLVQV
VREETLELGLLEPGLASMTQNLEPLLKKQGDWALPVAKLAIIRVGLAVVGSVLGAFLTFPGLR
LAQTHRDAITMSEDRPMQLFLLHTSFLSPLFILWLWTKPIARDFLHQPPFGETRFSLLSDSA
FDSGRLWLLVLCLRLAVTRPHLQAYLCLAKARVEQLRREAGRIEAREIQQRVVRVYCYVT
VVSQYLTPLILTLNCTLLKTLGGYSWGLGPAPLLSPDPSSASAAPIGSGEDEVQQTAAARI
AGALGGLTPLFLRGVLAYLIWWTAAQCQLLASLFGLYFHQHLGAS

FIGURE 145

FIGURE 146

GGTTCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGGCCGCGTATTATTAACTGGCTT
 AATCTGAAGGTTCTCAGTCAAATCTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTGCTTAAAGGAGC
 TTGGCTGGTTTGGGCCCTTTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAATGAAGG
 CGCTTCTGTTGCTGGTCTTGCCTTGGCTCAGTCTGCTAACTACATTGACAAATGTGGGCAACCTGCACTTCTGT
 TATTCAGAACTCTGTAAGGTGCCTCCCCTACGGCCTGACCAAAGATTAGGAAGAGGGCGCTCAAAAGATGGCTG
 TCCAGACGGCTGTGCGAGCCTCACAGCCACGGCTCCCTCCCCAGAGGTTTCTGCAGCTGCCACCATCTCCTTAA
 TGACAGACGAGCCTGGCCTAGACAACCTGCTACGTGTCTCGGCAGAGGACGGGCGCCAGCAATCAGCCCA
 GTGGACTCTGGCCGGAGCAACCGAACTAGGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTAA
 AAAAATAAATCGAGCTTTGAGTGTTCTTCAAGGACAAAGAGCGGGAGTGCAGTTGCCAACCATGCCGACCAAGG
 GCAGGGAAAAATCTGAAAAACCACTGCCCTGAAGTCTTCCAAAGGTTGTACCACCTGATTCCAGATGGTGAA
 ATTACAGCATCAAGATCAATCGAGTAGATCCCACTCAAAGCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAAC
 CCCACTGGTCCATATCATTATCCAACACATTTATCGTGATGGGGTGATCGCCAGAGACGGCCGGCTACTGCCAG
 GAGACATCATTCTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTCACAACCTACGCTGTGCGTCTCCTGCGG
 CAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTTCGCCAGCAGGAACATGGACAGGCCCC
 GGATGCCTACAGACCCCGAGATGACAGCTTTCATGTGATTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGGAA
 TAAACTGGTGGCAAGGTGGATGAGCCTGGGGTTTCATCTCAATGTGCTGGATGGCGGTGTGGCATATCGA
 CATGGTCAGCTTGAGGAGAATCACCGTGTGTAGCCATCAATGGACATGATCTTCGATATGGCAGCCAGAAAG
 TGCGGCTCATCTGATTACGGCCAGTGAAGACGTGTTCACTCGTGTGCTGCCCGAGCTTCCGCGAGCGGAGCC
 CTGACATCTTTCAGGAAGCCGGCTGGACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGGAGCAACT
 CCCAAGCCCCCTCCATCCTACAATTACTTGTGATGAGAAGGTGGTAAATATCCAAAAAGACCCCGGTGAATCTCT
 CGGCATGACCGTCGCGAGGGGAGCATCACATAGAGAATGGGATTTGCCTATCTATGTGATCAGTGTGAGCCCCG
 GAGGAGTCATAAGCAGAGATGGAAGAATAAAAACAGGTGACATTTGTGGAATGTGGATGGGGTGAAGTGA
 GAGGTGAGCCGAGTGAGGCAGTGGCATTATTGAAAAGAACATCCTCGATAGTACTCAAAGCTTTGGAAGT
 CAAAGAGTATGAGCCCCAGGAAGACTGCAGCAGCCAGCAGCCCTGGACTCAAACCAACATGGCCCCACCCA
 GTGACTGGTCCCCATCTGGGTGATGTGGGTGGAATTACCAGGGTGGTGTATTAATGTAAGATATTGTATTA
 CGAAGAAACACAGCTGGAAGTCTGGGCTCTGCATGTAGGAGGTTATGAAGAATACATGGAACAAACCTTT
 TTTTCATCAAATCCATTGTTGAAGGAACACCAGCATACAATGATGGAAGAATTAGATGTGGTGATTTCTTCTTG
 CTGTCAATGGTGAAGTACATCAGGAATGATACATGCTTGCTTGGCAAGACTGCTGAAAGAACTTAAAGGAAGA
 ATTACTCTAACTATTGTTTCTTGGCCTGGCACTTTTATAGAAATCAATGATGGGTGAGAGGAAAAACAGAAAAA
 TCACAAATAGGCTAAGAAAGTTGAACACTATATTTATCTGTGAGTTTTATATTAAAGAAAGAAATACATTGT
 AAAAATGTGAGGAAAGTATGATCATCTAATGAAAGCCAGTTACACCTCAGAAATATGATTCCAAAAAATTA
 AAACCTACTAGTTTTTTTTCAGTGTGGAGGATTTCTCATTACTCTACAACATGTTTTATATTTTTCTATTCAAT
 AAAAGCCCTAAAACAATAAATGATTGATTGTATACCCCACTGAATTCAAGCTGATTTAAATTTAAAAATTT
 GGTATATGCTGAAGTCTGCCAAGGTTACATTATGGCCATTTTAATTACAGCTAAATATTTTTTAAATATGCA
 TTGCTGAGAAACGTTGCTTTTCATCAACAAGAATAAATATTTTTTCAAGGTTAA

MKALLLVLPWLSpanyIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGC PDGCASLTAT
 APSPEVSAATISLMTDEPLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSR
 FKKINRALSVLRRTKSGSAVANHADQGRESENTTapeVFPrLYHLIPDGEITSIKINRVDp
 SESLSIRLVGGSETPLVHII IQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLL
 RQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVRKVDFPGV
 FIFNVLDGGVAYRHGQLEENDRVLAINGHDLRYGSPESA AHLIQASERRVHLVVSQRVQRS
 PDI FQEAGWNSNGSWSPGPGERSNTPKLPHPTITCHEKVNIQKDPGESLGMTVAGGASHRE
 WDLPIYVISVEPGGVISRDGRIKTGDILLNVdGVELTEVSRSEAVALLKRTSSSIVLKALEV
 KEYEPQEDCSPALDSNHNMAPPDWSWSPWMMWLELPRCLYNCKDIVLRRNTAGSLGFCIV
 GGYEEYNGNKPFFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSGMIHACLARLLKELKGRi
 TLTIVSWPGTFL

111

CCAAAGTGATCATTTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT
GCACAGGGCAGCTTTACTTTACTCCAGCACCTTCTCTCCAGGCAAATGGTGCTGACCATCT
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGC
AATGTTTCAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC
AGGATCATGCTCTTCTACCACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGTGC
TCTCCCGAAGAGCCTGCTTTATCTCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG
GGTCAAGTACAACCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCTGCTTGGGTAC
CCATTGAGAAACTCTGCAAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAAACACAT
AATGTCGGTGCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTG
TGCAGACATTATGTTTAGGATGATTAGCCCTCTTGTTTTATCTTTTCAAAGAAATACATCC
TTGGTTTACACTCAAAGTCAAATTAATTTCTTTCCCAATGCCCACTAATTTTGAGATTC
AGTCAGAAAAATATAATGCTGTATTATA

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FIGURE 149

MKILVAFLLVLTIFGIQSHGYEVFNIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTT
IFDYKHGYIASRVLSRRACFILKMDHQNIPLNNLQWYIYEKQALDNMFSNKYTWVKYNPLE
SLIKDVDWFLLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

FIGURE 150

GGCACGAGCCAGGAAGTCTAGGAGGTTCTCACTGCCCCGAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGGCTGTTCTGCTTGGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCTTGAAGTTTTCCCAAAG
GCCGCTGGGTGCTCATAACCTGCTGTGCACCCAGCCACCACCGCCCATCACCTATTCCCTC
TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGTGGTGAAGACCCACGAGCCGGCCTCCTT
CAACCTCAACGTCACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCGTCCT
CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
CCAGTGTCTGAGCTGCGGGCCAACCTTCACTCTGCAGGACAGAGGGCAGGCCCCAGGGTGA
GATGATCTGCCAGGCGTCTCGGGCAGCCACCTATCACCAACAGCCTGATCGGGAAGGATG
GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCTGCCG
AGCCAGACATCGGACTGGTTCTGGTGCCAGGCTGCAAACAAGCCCAATGTCCAGCACAGCGC
CCTCAGTGGTGCCCCAGGTGGTGACCAAGAAGATGGAGGACTGGCAGGGTCCCCCTGGAGA
GCCCCATCCTTGCCCTGCGCTCTACAGGAGCACCCGCCGTCTGAGTGAAGAGGAGTTGGG
GGGTTCAGGATAGGGAATGGGGAGGTGAGGAGCGCAAAGCAGCAGCCATGTAGAATGAACC
GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCCTGTTCGTATTGGA
GTTTCATGCAAAATGAGTGTGTTTTAGCTGCTTGGCCACAAAAAAAAAAAAAAAAAAAAA

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FIGURE 151

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVPKGRWVLITCCAPQPPPPITYSL
CGTKNIKVAKKVVKTHEPASFNLVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELRANFTLQDRGAGPRVEMICQASSGSPPITNSLIGKDQVHLQQRPCHRQPANFSFLP
SQTSDWFWCQAANNANVQHSALTVPVPPGGDQKMEDWQGPLESPIALPLYRSTRRLSEEEFG
GFRIGNGEVRGRKAAAM

Signal Peptide:

amino acids 1-18

N-glycosylation Sites:

amino acids 86-89, 132-135, 181-184

FIGURE 152

GGTCCTTA**AATG**GCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTG
CTGTCCGGCTGGTCCCGGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGT
CATCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGA
CTTTTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCACTGCCCTGGGGAAGAAA
CTAAATGTCAACGCGCTGGAAAGCACAGAACCCAGTACTGAGAGAGGTGGTGGACATACT
TACAGAGCAACTGCGTGACATTAGCTGGAGAATTACACACCCAAGGAACCCCTCACCTGC
AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGT
TTCGATGGGCAGATCTTCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC
TGGAGCCAGAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATT
ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACC
CTGAGCCAAAGTGCAGGAGCACCCTCGCCATGTCTCAGGCACAACCCAACCTCAGGGCCAC
AGCCACCACCTCATCCTTTGCTGCCTCCTCATCATCCTCCCTGCTTCATCCTCCCTGGCA
TCTGAGGAGAGTCCTTTAGAGTGACAGGTTAAAGCTGATACCAAAGGCTCCTGTGAGCAGG
GTCTTGATCAAACCGCCCTTCTGTCTGGCCAGCTGCCCACGACCTACGGTGTATGTCCAGT
GGCCTCCAGCAGATCATGATGACATCATGGACCCAATAGCTATTCACTGCCCTGATTCCCTT
TTGCCAACAATTTTACCAGCAGTTATACCTAACATATATGCAATTTTCTCTTGGTGCTACC
TGATGGAATTCCTGCACTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTC
TCTTTTGTGGAAAATCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAATGATATT
GTCAGTAAATAATCACGTTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCTGAAAGAG
AATTTTAAATTATTTAATAAGAAAAAATTTATATTAATGATTGTTTCTTTAGTAATTTAT
TGTTCTGTACTGATATTTAATAAAGAGTTCTATTCCCAAAAAAAAAAAAAAAAAA

FIGURE 153

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTFL
HYDCGNKTVTPVSPGLGKLNVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQAR
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMS FHYFS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLLILCCLLIILPCFILPGI

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

FIGURE 154

GGGAAAGCCATTTGAAAACCCATCTATACAAACTATATATTTTCATTTCTGCTGCTAGCTG
CCTTGGGCTCACAATTTTCATTCTGTTTTCTGACTTTCAAGTTATATACCGTGGA**ATGGAG**
TTGATCCCAACCATAACATCGTGGAGGGTTTAAATTTTGGTGGTAGCCCTCACCCAATTCTG
GTGTGGCTTTCCTTTCAGAGGATTCCACCTTCAAATCATGAACCTCTGGCTGTTGATCAAAA
GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAGAAGCTAGCAGAAGAC
TCAACCTGGCCTCCCATAAACAGGACAGATTATTCAGGTGATGGCAAAAATGGATTCTACAT
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCTCAAATTGGGAGGCCAAC
CCACAGAACAGCATTTCTGGGCCAGGCTG**TAA**TCAGAATTGTCGTCGTACATGCTCAACAGC
ATTGCTTTTTTCCCCAAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCTTACCTTT
CCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATTAAACCTTGCAGCAAGGGACC
TTAGATAGGCTTATCTGACTGTATGCTTTACCAATGAGAGAAAAAATGCATTTCCCTGTAT
CATCCTTTTCAATAAACTGTATTCAATTTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 156

GTTCTCCTTTCCGAGCCAAAATCCAGGCGATGGTGAATTATGAACGTGCCACACCATGAAG
 CTCTTGTGGCAGGTAACCTGTGCACCACCACACCTGGAATGCCATCCTGCTCCCGTTGCTCTA
 CCTCACGGCGCAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGCCTCAGCCGGGCCCC
 AGAACTGCCCCCTCCGTTTGTCTGCTGCAGTAACCAAGTTCAGCAAGGTGGTGTGCACGCGCCGG
 GGCTCTCTCCGAGGTCCCGCAGGGTATTCCCTCGAACACCCGGTACCTCAACCTCATGGAGAA
 CAACATCCAGATGATCCAGGCGGACACCTTCCGCCACCTCCACCACCTGGAGGTCTTGCAGT
 TGGGCAGGAACCTCCATCCGGCAGATTGAGGTGGGGGCCTTCAACGGCCTGGCCAGCCTCAAC
 ACCCTGGAGCTGTTCGACAACTGGCTGACAGTCATCCCTAGCGGGGCCTTTGAATACCTGTC
 CAAGCTGCGGGAGCTCTGGCTTCGCAACAACCCCATCGAAAGCATCCCCTCTTACGCCTTCA
 ACCGGGTGCCCTCCCTCATGCGCCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT
 GAGGGAGCTTTTGAGGGGTGTTCAACCTCAAGTATCTGAACCTGGGCATGTGCAACATTAA
 AGACATGCCCAATCTCACCCCCCTGGTGGGGCTGGAGGAGCTGGAGATGTACAGGGAACCACT
 TCCTGAGATCAGGCCTGGCTCCTTCCATGGCCTGAGCTCCCTCAGAAGCTCTGGGTCTATG
 AACTCACAGGTCAGCCTGATTGAGCGGAATGCTTTGACGGGCTGGCTTCACTTGTGGAAC
 CAACCTTGGCCCAACAATAACCTCTCTCTTTGCCCCATGACCTCTTTACCCGCTGAGGTACC
 TGGTGGAGTTGCATCTACACCACAACCCCTTGAACCTGTGATTGTGACATTCTGTGGCTAGCC
 TGGTGGCTTCGAGAGTATATACCCACCAATTCCACCTGCTGTGGCCGCTGTCTGCTCCCAT
 GCACATGCGAGGGCCGCTACCTCGTGGAGGTGGACAGGCCCTCCTTCCAGTGCTCTGCCCCCT
 TCATCATGGACGCACCTCGAGACCTCAACATTTCTGAGGGTCGGATGGCAGAACTTAAGTGT
 CGGACTCCCCCTATGTCTCCGTGAAGTGGTTGCTGCCCAATGGGACAGTGCTCAGCCACGC
 CTCCCGCCACCCAAGGATCTCTGTCTCAACGACGGCACCTTGAACCTTTTCCACGCTGCTGC
 TTTCAGACACTGGGGTGACACATGCATGGTGACCAATGTTGCAGGCAACTCCAACGCCTCG
 GCCTACCTCAATGTGAGCAGGCTGAGCTTAACACCTCCAACCTACAGCTTCTTACCACAGT
 AACAGTGAGACACCGGAGATCTCGCCTGAGGACACAACGCGAAAGTACAAGCCTGTTCCCTA
 CCACGTCCACTGGTTACCAGCCGGCATATACCACCTCTACCACGGTGCTCATTACAGACTACC
 CGTGTGCCCAAGCAGGTGGCAGTACCCGCGACAGACCACTGACAAGATGCAGACCAAGCCT
 GGATGAAGTCATGAAGACCACCAAGATCATCATTGGCTGCTTGTGGCAGTGACTCTGCTAG
 CTGCCGCCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCACCAGCAGCGGAGTACAGTC
 ACAGCCGCCCGACTGTTGAGATAATCCAGGTGGACGAAGACATCCAGCAGCAACATCCCGC
 AGCAGCAACAGCAGCTCCGTCCGGTGTATCAGGTGAGGGGGCAGTAGTGCTGCCCACAATTC
 ATGACCATATTAACATAACACCTACAAACCAGCACATGGGGCCCACTGGACAGAAAACAGC
 CTGGGGAACCTCTCTGACCCACAGTCACCACTATCTCTGAACCTTATATAATTACAGCCCA
 TACCAAGGACAAGGTACAGGAACTCAAATATGACTCCCCCTCCCCCAAAAACTTATAAAAT
 GCAATAGAATGCACACAAGACAGCAACTTTGTACAGATGGGGAGAGACTTTTCTTGTGTA
 TATGCTTATATATTAAGTCTATGGGCTGGTTAAAAAAACAGATTATATTAAATTTAAAGA
 CAAAAGTCAAAACA

00003601-114401
 10444-109600

FIGURE 157

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAASAGPQNCPSVSCSNQFSKVVCT
RRGLSEVPQGI PSNTRYLNL MENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS
LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSIMRLDLGELKKLEY
ISEGAFEGLEFNLKYNLGM CNIKDMPNLTPLVGLEELEM SGNHFP EIRPGSFHGLSSLKKLW
VMNSQVSLIERNAFDGLASLVELNLAHNNLSSLPHDLFTPLRYLVELHLHNPWNCD CDILW
LAWWLREYIPTNSTCCGRCHAPMHMRGRYLVEVDQAS FQCSAPFIMDAPRDLNISEGRMAEL
KCRTPPMSSVKWLLPNGTVLSHASRHPRISVLNDGTLNFSHVLLSDTGVYTCMVTNVAGNSN
ASAYLNVSTAE LNTSNYSFFT VTVETTEISPEDTTRKYKVPVTTSTGYQPAYTTSTTVLIQ
TTRVPKQVAVPATD TTDKMQTS LDEVMTTKIIIGCFVAVTLLAAAMLIVFYKLKRHQORS
TVTAARTVEIIQVDEDIPAATSAAATAAPSGVSGEGAVVLP TIHHDHINYNTYKPAHGAHWTE
NSLGNSLHPTVTTISEPYIIQTHTKDKVQETQI

FIGURE 159

MELGCWTLQLGLTFLQLLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVV
GYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLTDDFYVKGFYCAECRAGWYGGD
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD
GDNRDGQIIKRVCGNERPAPIQSIGSSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDG
TCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV
VSFFCNNSYVLSGNEKRTCQONGEWSGKQPICIKACREPKISDLVRRRVLPQVQSRETPH
QLYSAAFSKQLQSAPTKKPPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGK
WSGRAPSCIPICGIENITAPKTQGLRWPWQAAYRRTSGVHDGSLHKGAWFLVCSGALVNE
RTVVVAACHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAIILHPNYDPILLD
ADIAILKLLDKARISTRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTLRSG
VVSVDLSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEPR
WHLMGLVSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK

FIGURE 160

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTTCGAATCAGATTGGAAAAGCTCAACTTGA
 AGCTTTCTTGCCCTGCAGTGAAGCAGAGAGATAGATATTATTCACGTAATAAAAAAC**AT**GGGC
 TTCAACCTGACTTTCCACCTTTCTACAAATCCGATTACTGTTGCTGTTGACTTTTGCCCT
 GACAGTGGTTGGGTGGGCCACCACTAAGTACTTCGTGGGTGCCATTCAAGAGATTCTTAAAG
 CAAAGGAGTTTCATGGCTAATTTCCATAAGACCCCTCATTTTGGGGAAGGGAACCTCTGACT
 AATGAAGCATCCACGAAGAAGGTAGAACTTGACAACCTGTCCTTCTGTGCTCCTTACCTCAG
 AGGCCAGAGCAAGCTCATTTTCAAACCATCTCACTTTGGAAGAGGTACAGGCAGAAAATC
 CCAAAGTGTCAGAGGCCGGTATCGCCCTCAGGAATGTAAAGCTTTACAGAGGGTCGCCATC
 CTCGTTCCCCACCGGAACAGAGAGAAAACCTGATGTACCTGCTGGAACATCTGCATCCCTT
 CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGGTAAAAAGT
 TTAATCGAGCCAACTCTTGAATGTGGCTATCTAGAAGCCCTCAAGGAAGAAAATTTGGGAC
 TGCTTTATATTCCAGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGA
 GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTG
 GATATTTTGGGGTGTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATCTCT
 AACAACTACTGGGGATGGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAG
 AATGAAAATTTCCGGCCCCCTGCCTGAAGTGGGTAATATACAATGGTCTTCCACACTAGAG
 ACAAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTTTACACCAAGTGTCACGAGTCTGG
 AGAACAGATGGGTTGAGTAGTTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATA
 TATCAACATCACAGTGGATTCTGTTTGGTGCA**TGA**CCCTGGATCTTTTGGTGATGTTTGG
 AAGAACTGATCTTTGTTTGAATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTA
 AGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTTCTTTTGTATTTTCTTAGCAGAGCT
 CCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTTCTTAGTCATTTTGATCATG
 AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGAT
 AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATAT
 TATGGGATAAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCT
 CGTCCAAGGTAGAAAGGTACGAAGATACAATACTGTTATTCAITTTATCCTGTACAATCATCT
 GTGAAGTGGTGGTGTGAGGTGAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCA
 GGACACAGTGAACCTTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTCCGGCTGCAAAGGCAG
 CAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCCCT
 TCCAGTGATGCCACCAGAGAATACATTCTCTATTAGTTTTTAAAGAGTTTTTGTAATAATGA
 TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACATATTAATAATAATAATA
 TGTCTATCAATACCTCTGTAGTAAAAATGTGAAAAGCAAAA

FIGURE 161

MGFNLTFFHLSYKFRLLLLLTCLTVVGWATSNYFVGAIQEI PKAKEFMANFHKTLILGKGKT
LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYPQECKALQRV
AILVPHRNREKHLMYLLEHLHPFLQRQQLDYGIIYVIHQAEKGKFNRAKLLNVGYLEALKEEN
WDCFI FHDVDLVPENDFNLYKCEEHPKHLVVG RNSTGYRLRYSGYFGGV TALSREQFFKVNG
FSNNYWG WGGEDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSR
VWRTDGLSSCSYKLVSVEHNPLYINITVDFWFGA

Important features:**Signal peptide:**

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

FIGURE 162

CGTGGGCCGGGGTCGCGCAGCGGGCTGTGGGCGCGCCCGGAGGAGCGACCGCCGAGTTCTC
 GAGCTCCAGCTGCATTCCCTCCGCGTCCGCCCCAGCTTCTCCCGCTCCGGGCCCCGCAATG
 GCCCAGGCAGGTGTGGTCGCGCCTCGGCCGCATCCTCTGGCTTGCCCTGCCTCCTGCCCTGGG
 CCGGCGAGGGGTGGCCGACGGCCTGTATGAATCAATCTCACCCGATAGCCCTGCCACCA
 CGGGAGCGGTGGTGACCATCTCGGCCAGCCTGGTGGCCAAGGACAACGGCAGCCTGCCCTG
 CCGCTGACGCCCCACCTTACCGCTTCCACTGGATCCACACCCCGCTGGTGTCTACTGGCAA
 GATGGAGAAGGGTCTCAGCTCCACCATCCGTGTGGTGTGGCCACGTGCCCGGGGAATTCCCG
 TCTGTGTCTGGGTCACTGCCGTGACTGCTGGATGTGCCAGCCTGTGGCCAGGGGCTTTGTG
 GTCTCCCATCATCAGAGTTCTCGTGGGGGACCTTGTGTGTACCCAGAACACTTCCCTACC
 CTGGCCAGCTCCTATCTCACTAAGACCGTCTGAAAGTCTCCTTCTCTCCACGACCCGA
 GCAACTTCTCAAGACCGCTTGTCTCTACAGCTGGGACTTCGGGGACGGGACCCAGATG
 GTGACTGAAGACTCCGTGGTCTATTATAACTATTCCATCATCGGGACCTTACCCTGAAGCT
 CAAAGTGGTGGCGGATGGGAAGAGGTGGAGCCGGATGCCACGAGGGCTGTGAAGCAGAAGA
 CCGGGGACTTCTCCGCCTCGCTGAAGCTGCAGGAACCTTCGAGGCATCCAAGTGTGGGG
 CCCACCTTAATTACAGACCTTCCAAAAGATGACCGTGACCTTGAACCTTCTGGGGAGCCCTCC
 TCTGACTGTGTGCTGGCGTCTCAAGCCTGAGTGCTCCCGCTGGAGGAAGGGGAGTGCCACC
 CTGTGTCCGTGGCCAGCACAGCGTACAACCTGACCACACCTTCAGGGACCTTGGGACTAC
 TGCTTCAGCATCCGGGCCGAGAATATCATCAGCAAGACACATCAGTACCACAAGATCCAGGT
 GTGGCCCTCCAGAAATCCAGCCGGCTGTCTTGTCTTCCCATGTGTACACTTATCACTGTGA
 TGTGGCCCTTCATCATGTACATGACCTGCGGAATGCCACTCAGCAAAAGGACATGGTGGAG
 AACC CGGAGCCACCTCTGGGGTCAGGTGCTGCTGCCAGATGTGCTGTGGGCCCTTCTGTCT
 GGAGACTCCATCTGAGTACCTGGAATTTGTCTGTGAGAACCACGGGCTGCTCCCGCCCTCT
 ATAAGTCTGTCAAACCTTACACCGTCTGAGCAGCTCCCCCTCCCCACCCCATCTCAGTGTAA
 CTGACTGCTGACTTGGAGTTCTGAGCAGGGTGGTGTGCACCCTGACCAGGAGGGGTTCAAT
 TGGCTGGGGCTGTGGCCCTGGATCATCCATCCATCTGTACAGTTACGCCACTGCCACAAGCC
 CCTCCTCTCTGTACCCCTGACCCCGAGCCATTCACCCATCTGTACAGTCCAGCCACTGACA
 TAAGCCCACTCGGTTACCACCCCTTGACCCCTACCTTTGAAGAGGCTTCTGTGAGGACT
 TTGATGCTTGGGGTGTCCGTGCTGACTCCTAGGTGGGCTGGCTGCCACTGCCATTCTCT
 CTCATATTGGACATCTGCTGTCCATTGGGGGTTCTCAGTTTCTCCCCAGACAGCCCTAC
 CTGTGCCAGAGAGCTAGAAAGAAGGTCATAAAGGGTTAAAAATCATAAAGGTTGTAC
 ACATAGATGGGCACACTCACAGAGAGAAGTGTGCATGTACACACACCCACACACACACACA
 CACACACACACAGAAATATAAACACATGCGTCACATGGGCATTTTCAGATGATCAGCTCTGTA
 TCTGGTTAAGTTCGGTTGCTGGGATGCACCCCTGCACTAGAGCTGAAAGGAAATTTGACCTCCA
 AGCAGCCCTGACAGGTTCTGGGCCCCGGCCCTCCCTTTGTGCTTTGTCTGTGAGTTCTTGC
 GCCCTTTATAAGGCCATCCTAGTCCCTGCTGGCTGGCAGGGGCTGGATGGGGGGCAGGACT
 AATACTGAGTGATTGCAGAGTGCTTTATAAATATCACCTTATTTTATCGAAACCCATCTGTG
 TGGCTACGCCTGTAATCCCAGCACCTTTGGGAGGCCGAGGCGGGTGGATCACGAGATCAGGA
 GATCGAGACCACCTTGGCTAACACGGTGAAACCCCGTCTCTACTAAAAAATACAAAAAGTT
 AGCCGGGCGTGGTGGTGGTGCCTGTAGTCCAGCTACTCGGAGGCTGAGGCGAGGAGATG
 GTGGCAACCCGGAGGCGGAGCTTGCAGTGAGCCAGATGGCGCCACTGCACTCCAGCCTGA
 GTGACAGAGCGAGACTCTGTCTCCA

FIGURE 163

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVWVTAADCWMCQPVARGF
VVLPITEFLVGD LVVTQNTSLPWSSYLTKTVLKVSFLLHDP SNFLKTALFLYSWDFDGTQ
MVTEDSVVYYNYSIIGTF TVKLKVVAEWEVEPDATRAVKQKTGDFSASLKLQETLRGIQVL
GPTLIQTFQKMTVTNLNFLGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYNLTHTRDPGD
YCFSIRAENIISKTHQYHKIQVWPSRIQPAVFAFPCATLITVMLAFIMYMTLRNATQQKDMV
ENPEPPSGVRCCQMCCGPFLLETPSEYLEIVRENHGLLPPLYKSVKTYTV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

FIGURE 164

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCAGCGATGGCACTGAGCTCCCAGATCT
GGGCCGCTTGCCTCCTGCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCCA
CAACAGACGGGACAACCTTGCAGAGCTGCAACCCCAGGACAGAGCTGGAGCCAGGGCCAGCTG
GATGCCCATGTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCCCATCTGCATTTTCTGCT
GCGGCTGCTGTCATCGATCAAAGTGTGGGATGTGCTGCAAGACGTAGAACCTACCTGCCCTG
CCCCCGTCCCCTCCCTTCTTATTATTCTGCTGCCCCAGAACATAGGTCTTGGAATAAAA
TGGCTGGTTCTTTTGTTCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AA

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FIGURE 166

CTGT CAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCTGGC
 CTGGATCTTCCACCATGTTCTGTGTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGC
 ATCTCCCTGACTGTCTCTTACCCCTCCTTCTCGTTTTATCATAGTGCCAGCCATTTTGG
 AGTCTCCTTTGGTATCCGCAAACCTACATGAAAAGTCTGTTAAAAATCTTTGCGTGGGCTA
 CCTTGAGAAATGGAGCGAGGAGCCAAAGGAGAAGAACCACCAGCTTTACAAGCCCTACACCAAC
 GGAATCATTGCAAAGGATCCCACTTCACTAGAAGAAGAGATCAAAGAGATTTCGTGGAAGTGG
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGCC
 GGAAGGAATGGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAAGTGG
 GAGTCTTGAACCTGCTGAGCAGAACCAATTATAACTTCCAGTACATCAGCCTTCGGCTCAC
 GGTCTGTGGGGTTAGGAGTGTGATTGCGGTACTGCTTTCTGCTGCCGCTCAGGATAGCAC
 TGGCTTTACAGGGATTAGCCTTTCTGGTGGTGGGCACAACCTGTGGTGGGATACTTGCCAAAT
 GGGAGGTTTAAGGAATTCATGAGTAAACATGTTCACTTAATGTGTTACCGGATCTGCGTGCG
 AGCGCTGACAGCCATCATCACCTACCATGACAGGGAAAACAGACCAAGAAATGGTGGCATCT
 GTGTGGCCAAATCATACCTACCGATCGATGTGATCATCTTGCCAGCGATGGCTATTATGCC
 ATGGTGGGTCAAGTGCACGGGGGACTCATGGGTGTGATTGAGAGGCCATGGTGAAGGCCTG
 CCCACACGTCTGGTTTGAGCGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAGAGACTGA
 CTGAACATGTGCAAGATAAAAGCAAGCTGCCTATCCTCATCTTCCAGAAGGAACCTGCATC
 AATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTGTAAATTGGAGCCAGTTTACCC
 TGTGTCTATCAAGTATGACCCTCAATTTGGCGATGCCTTCTGGAACAGCAGCAAATACGGGA
 TGGTGACGTACCTGCTGCGAATGATGACCAGCTGGGCCATTGTCTGCAGCGTGTGGTACCTG
 CCTCCCATGACTAGAGAGGCAGATGAAGATGCTGTCCAGTTGCGAATAGGGTGAATCTGC
 CATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGCCTGAAGAGGGAGAAGG
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAACCA
 AAGGACAGGAGCCGCTCCTTGAGCCCTGCCTCCAGCTGGCTGGGGCCACCCTGCGGGGTGCCAA
 CGGGCTCAGAGCTGGAGTTGCCGCCGCCGCCGCCACTGCTGTGTCTTTCCAGACTCCAGGG
 CTCCCCGGGCTGCTCTGGATCCCAGGACTCCGGCTTTCGCCAGCCGCAGCGGGATCCCTGT
 GCACCCGGCGCAGCCTACCCCTTGGTGGTCTAAACGGATGCTGCTGGGTGTTGCGACCCAGGA
 CGAGATGCCCTGTTTTCTTTTACAATAAGTCGTTGGAGGAATGCTCCATTAAAGTGAACCCCCA
 CCTTTGCACGCTGTGCGGGCTGAGTGGTTGGGGAGATGTGGCCATGCTCTTGTGCTAGAGAT
 GGGCGTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTGGGGGCGGCCACCCG
 CTCTCCAGGAAAGGCACAGCTGAGGCACTGTGGCTGGCTTCGGCCTCAACATCGCCCCAGC
 CTTGGAGCTCTGCAGACATGATAGGAAGGAACTGTCATCTGCAGGGGCTTTTCAGCAAATG
 AAGGTTAGATTTTTATGCTGCTGCTGATGGGGTTACTAAAGGGAGGGGAAGAGGCCAGGTG
 GCGCGCTGACTGGGCCATGGGGAGAACGTGTGTTCTGTAATCCAGGCTAACCTGAACCTCCC
 ATGTGATGCGCGCTTTGTTGAATGTGTGTCGCGTTTCCCCATCTGTAATATGAGTCGGGGG
 GAATGGTGGTGATTCTACCTCACAGGGCTGTTGTGGGGATTAAAGTGCTGCGGGTGAGTGA
 AGGACACATCACGTTCAAGTGTTCAGTACAGGCCCAACAAACGGGCACGGCAGGCGCTGAG
 CTCAGAGCTGCTGCACTGGGCTTTGGATTGTTCTTGTGAGTAAATAAACTGGCTGGTGAA
 TGA

FIGURE 167

MFLLLPFDSLIVNLLGISLTVLFTLLLVFIIVPAIFGVSF GIRKLYMKSLLKIFAWATLRME
RGAKEKNHQLYKPYTNGIIAKDPTSLEEEIKEIRRS GSSKALDNTPEFELS DIFYFCRKGME
TIMDDEVTKRFSAEELSWNLLSR TNYNFYI SLRLTVLWGLGV LIRYCFLPLR IALAF TG
ISLLVVGTTVVGYLPNGRFKEFMSKHVHLMCYRICVRALTAIITYHDRENRP RGGICVANH
TSPIDV IILASD GYYAMVGQVHGGLMGVIQ RAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ
DKSKLPILIFPEGTCINNTSVM MFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMV TYL
LRMMTSWAIVCSVWYLP PMTREADEDAVQFANRVKSAIARQGGLVDLLWDGGLKREKV KDTF
KEEQQKLYSKMIVGNH KDRSRS

167-168-169-170-171-172-173-174-175-176-177-178-179-180-181-182-183-184-185-186-187-188-189-190-191-192-193-194-195-196-197-198-199-200-201-202-203-204-205-206-207-208-209-210-211-212-213-214-215-216-217-218-219-220-221-222-223-224-225-226-227-228-229-230-231-232-233-234-235-236-237-238-239-240-241-242-243-244-245-246-247-248-249-250-251-252-253-254-255-256-257-258-259-260-261-262-263-264-265-266-267-268-269-270-271-272-273-274-275-276-277-278-279-280-281-282-283-284-285-286-287-288-289-290-291-292-293-294-295-296-297-298-299-300-301-302-303-304-305-306-307-308-309-310-311-312-313-314-315-316-317-318-319-320-321-322-323-324-325-326-327-328-329-330-331-332-333-334-335-336-337-338-339-340-341-342-343-344-345-346-347-348-349-350-351-352-353-354-355-356-357-358-359-360-361-362-363-364-365-366-367-368-369-370-371-372-373-374-375-376-377-378-379-380-381-382-383-384-385-386-387-388-389-390-391-392-393-394-395-396-397-398-399-400-401-402-403-404-405-406-407-408-409-410-411-412-413-414-415-416-417-418-419-420-421-422-423-424-425-426-427-428-429-430-431-432-433-434-435-436-437-438-439-440-441-442-443-444-445-446-447-448-449-450-451-452-453-454-455-456-457-458-459-460-461-462-463-464-465-466-467-468-469-470-471-472-473-474-475-476-477-478-479-480-481-482-483-484-485-486-487-488-489-490-491-492-493-494-495-496-497-498-499-500-501-502-503-504-505-506-507-508-509-510-511-512-513-514-515-516-517-518-519-520-521-522-523-524-525-526-527-528-529-530-531-532-533-534-535-536-537-538-539-540-541-542-543-544-545-546-547-548-549-550-551-552-553-554-555-556-557-558-559-560-561-562-563-564-565-566-567-568-569-570-571-572-573-574-575-576-577-578-579-580-581-582-583-584-585-586-587-588-589-590-591-592-593-594-595-596-597-598-599-600-601-602-603-604-605-606-607-608-609-610-611-612-613-614-615-616-617-618-619-620-621-622-623-624-625-626-627-628-629-630-631-632-633-634-635-636-637-638-639-640-641-642-643-644-645-646-647-648-649-650-651-652-653-654-655-656-657-658-659-660-661-662-663-664-665-666-667-668-669-670-671-672-673-674-675-676-677-678-679-680-681-682-683-684-685-686-687-688-689-690-691-692-693-694-695-696-697-698-699-700-701-702-703-704-705-706-707-708-709-710-711-712-713-714-715-716-717-718-719-720-721-722-723-724-725-726-727-728-729-730-731-732-733-734-735-736-737-738-739-740-741-742-743-744-745-746-747-748-749-750-751-752-753-754-755-756-757-758-759-760-761-762-763-764-765-766-767-768-769-770-771-772-773-774-775-776-777-778-779-780-781-782-783-784-785-786-787-788-789-790-791-792-793-794-795-796-797-798-799-800-801-802-803-804-805-806-807-808-809-810-811-812-813-814-815-816-817-818-819-820-821-822-823-824-825-826-827-828-829-830-831-832-833-834-835-836-837-838-839-840-841-842-843-844-845-846-847-848-849-850-851-852-853-854-855-856-857-858-859-860-861-862-863-864-865-866-867-868-869-870-871-872-873-874-875-876-877-878-879-880-881-882-883-884-885-886-887-888-889-890-891-892-893-894-895-896-897-898-899-900-901-902-903-904-905-906-907-908-909-910-911-912-913-914-915-916-917-918-919-920-921-922-923-924-925-926-927-928-929-930-931-932-933-934-935-936-937-938-939-940-941-942-943-944-945-946-947-948-949-950-951-952-953-954-955-956-957-958-959-960-961-962-963-964-965-966-967-968-969-970-971-972-973-974-975-976-977-978-979-980-981-982-983-984-985-986-987-988-989-990-991-992-993-994-995-996-997-998-999-1000

FIGURE 168

GCCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCCGCCCTCACCCGGACCCCTGGCCCTCA
CGTCTCCTCCAGGGATGGCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCTCCAC
ACCTGGCAGGCCCAGGCTGTTCACCATCCTGCCCCCTGGGCCTGGCTCCAGACACCTTTGA
CGATACCTATGTGGGTTGTGCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG
AAATGGCCCACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCAGGAGACCTGGGAGGAC
AAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCCAGAATGGAATAGCCATTATGGT
CTACACCAACTCATCGAACACCTTGTAAGGAGTTGAATCAGGCCGTGCGGACGGGCGGAG
GCTCCCGGGAGCTCTACATGAGGCACCTTCCCTTCAAGGCCCTGCATTTCTACCTGATCCGG
GCCCTGCAGCTGCTGCGAGGCAGTGGGGGCTGCAGCAGGGGACCTGGGGAGGTGGTGTCCG
AGGTGTGGGCAGCCTTCGCTTTGAACCCAAGAGGCTGGGGGACTCTGTCCGCTTGGGCCAGT
TTGCCTCCAGCTCCCTGGATAAGGCAGTGGCCACAGATTGGGGAGAAGAGGCGGGGCTGT
GTGTCTGCGCCAGGGGTGCAGCTAGGGTACAATCTGAGGGGCTCCTCTCTGCCCCCTG
GAAGACTCTGCTCTTGGCCCCCTGGAGAGTCCAGCTCTCAGGGGTGGGCCCTTGAAAGTCCA
ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG
CAGCCTTGAGAAGCAAGAACATGGTTCCGGACCCAGCCCTAGCAGCCTTCTCCCAACCAGG
ATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACCTGCTATGTGATGGGACTTCCT
GGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGAGACA
TGAGATTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA

FIGURE 172

CTGGTTCCCCAACATGCCTCACCCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC
TCTGGACCCGTGAAAGAGCTGGTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTC
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCACCATAC
AGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA
GATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGT
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG
ACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCT
GGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAG
AAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCTGTGACGAGAACTTCTCAAGCCCC
ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCCTCCT
GTGCTCCTGTTGGTGCCCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTC
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGCGGAA
ACTCCTAACATATGCCCCCATCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA
TAGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAA
AGATGGAATAATCCCCACTACTGCTCACGATGCCAGACACCAAGGCTATTTGCCTATGAG
AATGTTATCTAGACAGCAGTGCCTCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAAAAA

FIGURE 173

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAAATGAAGATGCTGCTGCT
GCTGTGTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA
ACTTTAATGTAGAAAAGATTAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA
GAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTGGAGCAAATCCATGTCTTGAGAA
TTCCTTAGTTCCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGGTTG
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAACGAAAAGGATGGGGA
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAA
GGTTTGCACAACATATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT
GCCAATCGCTGCCCTCCAGGCCCGAGAATGAAGAATGGCCTGAGCCTCCAGTGTGAGTGGAC
ACTTCTCACCAGGACTCCACCATCATCCCTTCCTATCCATACAGCATCCCCAGTATAAATTC
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCCAGTCTATCAACATGTTACC
TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTTGATACACCCCTTGACAAT
TTTTCATGAAATTATTCCTCTTCCTGTTCAATAAATGATTACCCTTGCACTTAA

FIGURE 175

GGCTCGAGCGTTTCTGAGCCAGGGTGACCAATGACCTGCTGCGAAGGATGGACATCCTGCAA
TGGATTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG
TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTC
CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG
AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTCAGTGTGATCA
CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTC
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA
CATTCATCCAGAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG
GTTTCAATAAACCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCAC
TTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTTCTCAGTATTTTtaggtctattgct
TGTGGAATTCTGGAGGTCCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTTGGCTGTC
TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAAATGGGAATAAAATGTAAGTA
TCAGTAGTTTGAAAAAAAAA

MTTCCEGWTSNCGFSLVLVLLLVGVNLAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA
IPATMTSLTARKRACNNRTGMFLSSFFSVITVIGALYCLISIQALLKGPLMCNPSNSNA
NCEFLSKNISDIHPESFNLQWFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSSEENKHL
IHFVFLGLLLVGLILEVFLGLSQIVIGFLGCLCGVSKRRSQIV

FIGURE 177

GTCGAATCCAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCT
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCT
GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC
CAAGTTGCCAACTTAATCCACCTCCAGAAGCTCTTGACGCCAAGTTGGAAGTGAAGCACTG
CACCGATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGAAATAGTGAA
AAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTCAACGACACC
CTGATCTTCACTAAAAATGTAAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

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FIGURE 178

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLQVAKLNPPPEALAAKLEV
KHCTDQISFKKRLSLKKSWWK

2011-03-03 10:00:00

FIGURE 179

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG
GAGCAGATCCGTGGGCTGCAGACCCCGCCCCAGTGCCCTCTCCCCCTGCAGCCCTGCCCCTC
GAACTGTGACATGGGAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG
AAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAACTGCAG
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCAC
TCATCACTCCAGGCTCTGCCACTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGA
AGCCTAACACTGGCCCCAGCACCTCCTCCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC
TCTCCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGCTTCTTTATGAATTAACTCG
CCCCACCACCCCTCA

FIGURE 181

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGGATGTCGCTGCTGAGCCTGCCC
 TGGCTGGGCCTCAGACCGGTGGCAATGTCCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTC
 CTGGCTACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAAGTCCCGCCGGCTCC
 AGTGTTTTCCACAGCCCCAAAACGGAAGTGGTTTTGGGGTCACCTGGGCCTGATCACTCCT
 ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTCGGCCACCTATTCCCAGGGCTTTACGGT
 ATGGCTGGGTCCCATCATCCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCA
 CCAATGCCTCAGCTGCCATTGCAACCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGG
 CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGAC
 GCCCGCCTTCCATTTCACATCCTGAAGTCTATATAACGATCTTCAACAAGAGTGCAAACA
 TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCGCTCTGGACATGTTTGAG
 CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACAGCCATTG
 TCAGGAGAGGGCCAGTGAATATATTGCCACCATCTTGAGCTCAGTGCCCTTGTAGAGAAAA
 GAAGCCAGCATATCCTCCAGCACATGGACTTTCTGTATTACCTCTCCCATGACGGGCGGCGC
 TTCCACAGGGCCTGCCGCCTGGTGCATGACTTCACAGACGCTGTCATCCGGGAGCGGCGTGC
 CACCCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAAAGCCAAGTCCAAGACTTTGG
 ATTTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTGATGAGGAT
 ATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCCTCTC
 CTGGGTCCTGTACAACCTTGCGAGGCACCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGC
 AAGAGCTTCTGAAGGACCGCATCCTAAAGAGATTGAATGGGACGACCTGGCCCAGCTGCCC
 TTCCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATCTCCCG
 ATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTGCC
 TCATCGATATTATAGGGTCCATCACAACCCAAGTGTGTGGCCGGATCCTGAGGTCTACGAC
 CCCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTACCTCTGGCTTTTATTCTTTCTC
 CGCAGGGCCAGGAAGTGCATCGGGCAGGCGTTGCCATGGCGGAGATGAAAGTGGTCTGAG
 CGTTGATGCTGCTGCACTTCCGGTTCTTGCCAGACCACACTGAGCCCCGAGGAAGCTGGAA
 TTGATCATGCGCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCCGTAATGTAGGCTTGCA
GTGACTTTCTGACCCATCCACCTGTTTTTTTGAGATTGTGATGAATAAACCGGTGCTGTCAA

FIGURE 182

MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFPQPPKRNWFWG
HLGLITPTEEGLKDSTQMSATYSQGFTVWLGPPIIPFIVLCHPDTIRSITNASAAIAPKDNLF
IRFLKPWLGEGILLSGGDKWSRHRRLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGS
SRLDMFEHISLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY
LSHDGRRFHRACRLVHDFDPAVIRERRRTLPTQGIDDFKDKAKSKTLDFIDVLLLSKDEDG
KALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEW
DDLAQLPFLTMCVKESLRLHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW
PDPEVYDPFRFDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHT
EPRRKLELIMRAEGGLWLRVEPLNVGLQ

000000 111111 000000

FIGURE 185

GAACATTTTtagTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT
GGGGTTGCTGGTTTAAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA
CCACCTCCGCCAGGAAGTGCAGGCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCCCC
AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT
CCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGGAAGATGGAGGTCAAGCAGA
AGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGT
CAGGGGTTcAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGG
GAAGAGGCCAAAGAGGCCCCAGCCGACAAGTGATCGCCCACAAGCCTTACTCACCTCTCTCT
AAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTA
CAAGCTCAGGAGGCGAATAAATGTTCAAAGTGA

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FIGURE 186

MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDG
GQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

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FIGURE 187

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCCTCGTCCAGTACCTC
GTGAACCCCGGGGTGCTCCGCACGACCCAGATGTCAAGAATATGAACACGTGGCTGCTGT
TCCTCCCCCTGTTCCCGTGTCAGGTGCAGACCCTGATAGTCGTGATCATCGGGATGCTCGTG
CTCCTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCT
GAGTATGTCCCCACCCTAAGCCCCGATCCCCCAAGGTGGGTGGTTCAGAGCTGCTCATC
TTACACCTCTACTTGAGTATGTCCCTAACCCCTGAGCCCCACGCCTGGGGCCAGAGTCTTT
GTCCCCCGTGTGCGCATGTGTTCAAGGTTCAGCTCTCCAGAAGTGAGATCATGGACAAAA
GGGCAATCACAGGAAGAAATTAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAAC
TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAATGTTTCTGAG
GACAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT
CCAAAAACACAAGTAGAAATTTAACAATGAAATATATTACAGGCAGGTACCCACTAACC
AACAACTGAAGCGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGT
AGTCATGTTGCTGAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT
AACAAACACCTCCCTGCTCCTGGCACCAGCCGTTTGGTTCATGGTGGGCCAGCTGCAAAGCG
TCTTCCATTCTCTGGGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGGTTTCTGTGGAC
ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCA
ACCCCTGGTTCAGGGCAGAGGGAGTTGGGTGGGTTCAGGCTCTGGGCTCACCTCCATCTCCAGA
GCATCCCCTGCTGCAGTTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCACCAAGA
GCCTCCTTGTTCATAACCACAGTTACCCTACAAACCACTGTCCCCACACACCCCTGGGGAT
GTTTTTAAACACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCTGAGGGTTGA
ATTTTTTTTAAATGAAAGTGCAATGAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

GGAGTGCAGATGGCATCCTTCGGTTCCTCCAGACAAGCTGCAAGACGCTGACCATGGCCAAAG
ATGGAGCTCTCGAAGGCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT
ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG
TGCCCAAGCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCCTG
GATGGAGATACCAACACATCCACCCAGGAGGTGGTACAATACTGAGGAGCTGGGGATG
CCGGTTCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAACTGTGGAAG
AACCAGGGGAGAGGTGCCGAAGTTTCATTGAACTTACACCACCAGCCAAGAGAGGTGAGAAA
GGACTACTGGAATTTGCCACGTTGCAAGGCCCATGTCACCCCACTCTCCGATTTGGAGGGAA
GCGGTTGATGGAGAAGGCTTCCCTCCCCCTCCCCCTTGGGGCTTTGTGGCAAAAAATCCTA
TGTTTATCCTGGGAACGCAGATCACCTACATCGGACTTCAATTATCAGCTTCTCTCTGCT
ACTAACAGACTTGCTACTCTACTGGGAACCTGCCTGTGGGCTCAAAGTGAAGCGCTTTGCTG
CTGTTTCTCTGTCTGTGAGGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAGTC
TCCAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGAATTATGGCTG
GGCCTTCTACATGGCCTGGCTCTCCTTCACTGCTGCATGGCGTCGGCTGTCAACCACCTCA
ACACGTACACCAGGATGGTCTGGAGTTCAAGTGAAGCATAGTAAAGAGCTTCAAGGAAAAAC
CCGAAGTGCCTACCACATCACCATCAGTGTTCCTCGCGGGCTGTCAAGTGCAGCCCCAC
CGTGGGTCTTTGACCAGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAG
GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGGATTTCAAAGAGGGGCCAGCCAGGAGCTG
AAAGAAGCAGTTAGGTCATCTGTAGAGGAAGAGCAGTGTAGGAGTTAAGCGGGTTTGGGGA
GTAGGCTTGAGCCCTACCTTACAGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCG
TCTCTTGAGCATGGTTTTTTAGAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC
CTAAGGGATTCTGGGTGCCACTGCTCTCTTTTCTCTACAGCTCCATCTGTCTTCAACCAC
CCACATCTCACACATCCAGAATTCCTTCTTTACTGATAGTTTCTGTGCCAGGTCTTGCGC
TAAACCATGGAGATAAAAAAGAGTAAAAACACTTCCCGACCTTAAGGATCTGAAA

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FIGURE 190

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWVFVGTQKVPKPLCEKGLAAKCFDMP
VSLDGDNTNTSTQEVVQYNWETGDDRFSSFRSGMWLSCEETVEEPGERCRSFIELTPPAKR
GEKGLLEFATLQGPCHPTLRFGGKRLMEKASLSPPLGLCGKNPMVIPGNADHLHRTSIHQL
PPATNRLATHWEPCLWAQTERLCCCFLCPVRSPGDGGPHDVFTSLPSDCQLGSRRLETTCL
LWLGLLHGLALLHLLHGVGCHHLQHVVHODGAGVQVQA

SECRET

FIGURE 191

AACTGGAAGGAAAGAAAGAAAGGTCAGCTTTGGCCCAGATGTGGTTACCCCTTGGTCTCCTG
TCTTTATGTCTTTTCTCCTCTTCCTATTCTGTCATCTCCCTCACTTAAGTCTCAGGCCTGTCA
GCAGCTCCTGTGGACATTGCCATCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATG
TTATGGATGTTTCCACCAACCAGGCTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGT
GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG
AGATGGCACAGGTGACCACGCAGAAGCCACCAGAACTTGCCTGCCCTATTCCTCCTCCCAA
GTCTGTTCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCCAATGGCATTACAGAGAAAG
CAATCTGTGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGT
AGCCACCTCCCTGTGAGCCAGTATTAACATGTCCCCTTCCCCCTGCCCGCCGTAGATTGAG
GACATTGCCCCCTGTGTGCCACCAACAGGACTTTCCTTGGCTTGGCATCCCTGGCTCT
CTCCTGGTACCCAGCAAGACGTCTGTTCAGGGCAGTGTAGCATCTTTCAAGCTCCGTTACT
ATGGCGATGGCCATGATGTTACAATCCCACCTGCCCTGAATAATCAAGTGGGAAGGGGAAGCA
GAGGGAAATGGGGCCATGTGAATGCAGCTGCTCTGTCTCCCTACCCTGAGGAAAAACCAAA
GGGAAGCAACAGGAACCTTCTGCAACTGGTTTTATCGGAAAGATCATCCTGCCTGCAGATGC
TGTTGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAA
ATAGAACAGTCTGCTGGGAGTCAGACCTGGAATTCTGATTCCAACTCTTTATTACTTTGGG
AAGTCACTCAGCCTCCCCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGG
AACCAAGGAAACTAACAATGTAGGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCC
CATGCCACCAAAACAATAAAACAAAATCTCTAACACTGAAA

000304-1100

FIGURE 192

MWLPLGLLSLCLSPILSSPSLKSQACQQLLWTLPSPLVAFRANRTTYVMDVSTNQSGSME
HRNHLCFCDLYDRATSPPLKCSLL

GTAGCGCGCTCTTGGGCTCTCCGGCTGCGCGCTGCTGCGCGCGCGCGCTCGGGTCGTGGAGCCAGGAGCGCACTCA
CCGCTC**ATGG**CGAGCAGTCAAAAGCTTTGATTAGTTTGTCCTTTGGAGGAGCAATCGGATGATGTTTTTGATGCTT
GGATGTGGCCCTTCCAAATATACAAATAACATGGCCCTCTTTGTTCTATTTTTTACATCCTTTCACTTATCC
ATACTGCATAGCAAGAAGATTAGTGGATGATACAGATGCTATGAGTAACGCTTTGAAGAACTTTGCCATCTTTC
TTTCAACAGCGGCATTCGTGCTGACGTTTTGGACTCCCTTATTTGATTTGTCAGAGACATCTGATTGAGTGGGA
GCTTTGTGCATTTGTTCCTCAGAGAAACACAGCATCTTTTGAACATATACTAGGCTTTTTCTTGGTCTTTGGAAG
CAATGACAGCTTCAGCTGGCAGCAGTGG**TGA**AAAGAAATTTACTGAACATTTGCAAAATGCACTTCCTGTCATT
TTGTGCCATTACGACAGCAGGAGATGGGGCAGTTATGCTGAATGGTATAGCAAGCTCTTGGGGGTTTTTTA
GGTGCTCCCTTCTCACTTTTATTGTAAGCATATACATTTTTCACAGAGACTTGCTGAAGGATTAAGAAAGTTTTCT
CTTTTGGAAAGGCTTGACTGATTTCACTATCTATAGTAGCTTTTTGGTGGTCTGCTGCTGATTTAAATAT
TTATGTTTCTTTCTGTAGTGTGATTTTTTTGGAATCAATATGCAATGTTAAACACTTTTTTAATGTAATCA
TTTGATTTGGTAGGAAATTCAGAAATTCGCGCGGCTCTATTATCTGTCAGATACATCTTTCTCTAAAAATATT
TAGCCTCCATTTATACAAAAAATTATAAAATAAGTTTTCACTGTCAGGATGACATCACTCCCAATGGTATG
CAGACATACAGACGGTTGGCATAGTTATAGACTGTATACAGTCAATATAGCTGCATTTATACCTCAGAG
GGGCCAAGTGTAAATGGCCCATGCCCTCCGTTAGGGTGTGGTTTTCTTGTGATGCTGTGATGAAATGTTTTGGGATGT
AAAATATTTTAGGAATTGCTACAGAGGAGTGCTTTTCTTCAATGTTTGAAGAATATTATGTTAACTTTA
AGGTAAAGGTTGTAAACAAATTTTGGAGTAAGTTTTATTTATGTTTATAATGTTAGAGTGAGTGCAGATGT
GGGAAGAAATGACATTTGAATTTCCAGTTTTTGAATCTGTCTTATTTAGTGTGAAATTTGTATCCTCTAT
AACTCTTCATGTTTTACCTCTGTAAATGGACATACATGGAACCACTACTGATGAGGACAGAGCTGTGATTTGTGC
ATCATATATGCGAAAACCTTCTGCTCTCTCTCTTTGACTTTTGGTATGTTGATATATATACATAAAA
TAACTTTTCAAATATAGTTTAAATAACACTAGAAGTGTTTACTACCTGGAAGATTTGCTATGCCGATCAAT
CAGAGTGCCCCCTCCCCGCAAGGCCCTGGCCATGATAAACAAGTAACTTTGTAATCTACAGATAATCTACGTA
TAAACAGTTTTAAGATTTAGACATGGTAATAGTAGTCTTATTCTTAAGGTTATATCATATGTAATTTAAAG
TATTTTAAAGCAAGTTTTCTGTATACCTCTGAACCTGTTTGATTTTGAAGTTCACTCATATGATAGATCTGCTGTT
CCCTATAAAAGGCATTTGTGTGAGTAATGCAAGTAGGCAAGTCAGCATAATAGCACTCAGAAACAT
ACCTGACCAAAAATTCGCAGTAACCGGACATCAAAATTTAGTAGTGTGCTTTACATCTAATAAATATCAGGA
CTTTTTTCAGGAGTGGGTTATAAAACATTTCAAGTGGTCTGACAGATTTTTGTTAAGGATATTTGTTGTATG
TTTATTCAGTACTTACATAAAATATTTCGCCATCAGCCAAAACCTCAGTAATCATGACAGCTGCTGTGTT
TTTATGAAGTTTTATTTCAAGAAATGGGAATAAATTTGGGATTTGTCAGTTTTTTACTAAAGATGCCATA
AGCCAGAGGTTTTTATGGCTCAATTTAGGCATGACTTTTAGATATGAGATCGGGAAGCAGGACGAATATCG
CGGTGTGGCTGGAGCCTTCCCACTGGAGGCTGAAAGTGCCCTGTGGTATATATATGTTCTCAGATTTCAAGAGGAA
GGTCGACGTACACAGATTTAGAGAGCTGGTGACAGATTTGGGAACCTCTTTGTGCTGTGATCTACGACATTT
TTTTTTGCAGGAAGTGCAATCTCTGCTCTCCCTATTTCTTGTGATGTCAGTGCAGTGCACTGCTACTG
TTTTATCCATCTGGCCACAGACTTTTTCTAACAGCTGCGTATTATTTCTATATCAATTTGCAATGGCAGAT
GTGTCTTGACCTTTGTATCTAGCTTGACATAGTGTGCTCTGATTTCTAGGCTATTTACTTGAGATATGAAT
TTTCCATAGAATATGCAGTATACACAAATCCACTTCTCTATGGAAGAAAACCTTTGATGATGAACAAATA
AGATTTTAAATATCTATTTTAAAAAATAA

FIGURE 195

CCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCC
 CACGCGTCCGGTGCAGCTCCGCCGCCACACTGCCCTGGTGGAGGGGAAGGAGGCCCGGGCGCTCTCGCGCTCC
 CGCGCGCGCTCCGACCTCCGCCCG
 TCTGCAGCTGCCCGGGGGCGGAATGGCAGGCTGTTCCGCGGAGTAAAAGGTCGGCGCGCTGAGTGGCTCT
 CAATGACGGACATTAACAGACTTGCAGATCCTGGGGAGTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
 AAGCTCAGAGTCCGAACTGCGAGAGGGAAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
 GAAACTTGGGGTCTTGAAGTCCGCTGCCATCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
 GAGACATTTGCGCGCTGCCATCGCTCCCG
 GCCTGCATATATATAGCTGCACACAAGGGAGCAGCTGAATGGAGGTTGTCACTCTCTGGAAAGGATTCT
 GACCGAGCGCTTCAATGGACATTTCCAGTCTCTCTGGAAAGATTCTCGCTAATGGATTTCCTGCTGCTCGGT
 CTCTGTCTATATCTGGCTGCTGAGGAGGCGCTCGGGGGTGGTCTTGTGTCTGCTGCGGGGCTGCTTTCAGATGCT
 GCOCGCGCGCGCGCGCGCGGCTGCCGAGCTGTGCCGTGCGAGGGGGGGTCTGCTGACTGCGAGGCGCTCAAC
 TCACCGAGGCGCGCGCGCGCGCGCTGTCCGGCTGCTGGGCTGTCCCTGCGCTACAAAGCGCTCTCGGAGCTGCGC
 GCGCGCGAGTTTACGGGGTTAATGAGGCTCAGCTGGCTCTATCTGGATCACAAATCACATCTGCTCGTGAGGG
 GAGCGCTTTCAGAAATCGCGCGAGTTAAGGAACCTCAGCTGAGTTCCAAACAGATCACCAACTGCCCAACA
 CCACTTTCGGCGCACTGCCAGCTGCCGAGCTGGACCTCTCGTACAAACAGCTGCAGGCGCTCGCGCGCGGAC
 CTCTCTCCAGGGCTCGGGAAGCTCACCAGCTGCATATCGGGGCCAACCGCATCCAGTTTGTGCCCGTGCGCAT
 TTTCCAGGACTCGCGCGCTCAAGTTTTCGACATCGGATACAACTCAGCTCAAGAGTCTGGCGCGCACTCTT
 TCGCGCGCTTGTAAAGCTCAGCGAGCTGCACCTCGAGCACAAACGACTTGGTCAAGGTTGAATCTCGCGCGCACTCT
 CGCGCGCTCATCTCCCTGCACCTGCTGCTCGCTCGGAGGAACAGGTTGCCATTGTGTCAGTCTCGCGCGCT
 GGTTTTGAACCTTGGAGAAATGGAATTTGTCGGGCGAGGAGTTCAGTACATGAGCGCCCTGCTGTCGAGACCG
 TGCAGCACTCGAGTCTCGAGCTGCGAGCTCGAGCTCGAGTACATGAGCGCCCTGCTGTCGAGACCG
 AACTCTTGCAGAGCATCACTCGCTGCGCGGGAACCTTGGGATTCGCGCGCAACGTTGTGCCCTGAGCTCGTG
 GCTCAGCACTTCCAGGCGCTCAGATGGCAACTTGCAGTGCAGCGCGCGGAGTACGCACAGGCGGAGGACG
 TCTGTCAGCGCTGTACCGCTTCCACTGTGCGAGGATGGGGCGGAGCGCCAGCGCCAGCGCGCTGCTCTCGCG
 GTACCAACCGCGAGTGATCTGGGCGCGCTGCCAGCTCGCGCGCACCGCTCGCGGACGCGCGGGGAGGGGACGCA
 CGAGCACTTCGAGCTGCCAGCTGCCACCGTGGCTTTCCAGGCGCGGAGCACGCGGAGAACCGCGTGCAGATCCACA
 AGGTGTCACGGGCGACCTGGCCCTCATCTTCTCTCTCATCGTGGTCTGGTGTCTACGTGTCTGCGAAG
 TGTTTCCAGCGCGCTCAGCGCTGCCACCGTGCAGCAGTGCTTTGTACGAGCGGAGGAGCAAAAGCAGAAACAGAC
 CATGCTCATGATGGTGGCTGCATGTCTGCCAGGAATACAGTTGATTACAAACCGAACCATATTGAGGGAGCGCC
 TGGTGATCATCAACGAGTATGGCTCGTGTAACCTGCCACCGAGCGCGCGGAGGGAATGCGAGGTGGAATGTCC
 CAGTGGCTCTCAACCGATCGGCTACCAAAATACGCTGGGCGAGCGGGGACGGGCGCGCGCGCACCGCTGGGGT
 CTCCTTGTCTGTGCTGATATGCTCTTGACTGAAACTTTAAGGGGATCTCTCCAGAGACTTCACTTTATG
 TATCTTAAATTCATATGAGACTCTCTTCCCTCTTGAATCTGAGACTCTGAGACTCTGAGACTCTGAGACTCT
 TATCTTAAATTCATATGAGACTCTCTTCCCTCTTGAATCTGAGACTCTGAGACTCTGAGACTCTGAGACTCT
 ABCATCATCTATCTGAGACTCTTAAAGTCCATACGATTTCTATGAAAGCACTTGAAGAGGGAATCTGCAATC
 TGGGAGCTTAAAGCAAAATGATGACCATAGAAAGCTATGTTCTTACTTGTGTGTGTCTGTATGTTTCTCGG
 TTGTGTGTCTTTGAGGCAAGCAACGTTGTCTACACAAACGGGAAATTTAGCTACATCATTTATGCGCCCTGT
 GCCTTAGCTCTGGAGATTGGTGGGGGGAGGTGGGGGGAAACGCGAGGAATAGGGGAAAGTGGATGTTTAACT
 AAGGTTTGTGACACTTGAATCTTTTCTTCTCAAATTAATATCTTTAAGCTTCAAGAAAGCTGCTCTGACG
 CCTCTAAGCAAACTACTAAGCATTTAAAGAGAAATCTAAATTTTAAAGGTGTAGCACTTTTTTTTTTCTTCT
 CCACAGAGGGTGCTAATCTCATTTAGTGTGTGCTATCTGAAAGAACTTAAAGGCCAACAATCAGCTCTCGTCTG
 GGCATTTGATGGATTGACCTCCATTTGAGTACCTTCCAGCTGATTAAAGTTCAGAGTGGTATTGAGGTT
 TTTTGAATATTTATAGAAAAAAGTCTTTTACATGACAAATGACACTCTCACACGACTTATAGCCCTAGTA
 GTTTTTTATAGTTGGACGAGGGAAGCAGGTTAAATGAGACTGTCTCTGCTGCTCAGACTCAGAAAAATAGCAGT
 CCTGATGCTCAGATCTTAGCTTGATATTAATAGTTGAGCAGCTTACCCCAATGCACTTACAGCTTCCCAAG
 ACTACAAAGTCAACTCGCAAGGAAGGTTATTTCCACTAAAAGGAATAGTTTCTCAACCATTTAAAAAT
 TCTTCTGAACCTCAGCAACTAGAGCTTCTCTCTCTGCTCTCAAGAGGCGACATTTGGTATG
 ATTTAGCATCAACAACATATATGATATATGTAAGTAATCAGAGGGGCAATGCGACTTGTATTCTCCCA
 AGTTTTCTCAAGCAAGTACACAGATCTCTGGTAGGATTAGGGGCGACTTGTGTTTCCGGCTTATTTTCTCGA
 CTGTCAGCAAGTTTGTAGCTTCTATCTGACATGGCCGAGTGAACAGGGCACTGATGATCAGATGAGAT
 GGTAGAGGAACATCATCATACCTCTCAGAGAGAAATTAACAAAGAACAGAAATTAATCTGTTTGG
 AGCAAGAGTGTATATATTTTTCAGGGTGTCAAATAAAACATAAATTAATCTCTCTAGATGAGTGGCGATGTTG
 GCTGATTTGGGTCTGCCATTGACGAATGTCAAATAAAAGGAATAGCTAGAAATGACCAATTAATGTGCTT
 CTGAAATATATTTTGAATAGGTTTGAATGTCA

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 101111 1096660

FIGURE 196

MDFLLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPH
NLSGLLGLSLRYNSLSELRAQQTGLMQLTWLYLDHNNHICSVQGDAFQKLRRVKELTLSSNQ
ITQLPNTTFRMPNLRSDLSYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRIFQDCRS
LKFLDIGYNQLKSLARNSFAGLFKLTTELHLEHNDLVKVNFAHFPRLISLHSLCLRRNKVAIV
VSSLDWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRLTYIEPRIILNSWKSLSIT
LAGNLWDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDAVYAFHLCEDGAEPTSG
HLLSAVTNRSDLGPPASSATTADGGEGQHDGTFEPAVALPGGEHAENAVQIHKVVTGTMA
LIFSFLIVVLVLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNH
IEGALVIINEYGSCTCHQQPARECEV

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FIGURE 197

GTGCAAGGAGCCGAGGCGAGATGGGCGTCCTGGGCCGGGTCTGCTGTGGCTGCAGCTCTGC
GCACTGACCCAGGCGGTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTTCGCAGCCAA
CTGGAGCCAGAACCGGACCCCGTGCGCCGGCGCGCGCTTGAGTTCCCGGCGGACAAGATGG
TGTCACTCCTGGTGCAAGAAGGTCACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGAA
CTCGTCCTGGCTTCAGGAGCCGGATTTCGGCGTCTCAGACGTGGGCTCGCACCTGGACTGTGG
CGCGGGCGAACCTGCCGTCTTCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT
GGCGCTCTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCGTGCCCTGCCGC
CACGACGACGTCTTCTTTCCGCCTAGTGCCCTCCTTCGCGTGGGGCTCGGCCCTGGCGTAG
CCCCGTGCGTGTCGCGAGCATCTCGGCTCTGGGCCGGACGTTACGCGCGACGAGGACCTGG
CTGTTTTCTGGCGTCCCGCGCGGGCCGCCTACGCTTCCACGGGCCGGGCGCGCTGAGCGTG
GGCCCCGAGGACTGCGCGGACCCGTTCGGGCTGCGTCTGCGGCAACGCGGAGGCGCAGCCGTG
GATCTGCGCGGCCCTGCTCCAGCCCCCT

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FIGURE 199

ATCGCATCAATTGGGAGTACCATCTTCCTCATGGGACCAGTGAAACAGCTGAAGCGAATGTT
TGAGCCTACTCGTTTGATTGCAACTATCATGGTGCTGTTGTGTTTTGCACCTTACCCTGTGTT
CTGCCTTTTGGTGGCATAACAAGGGACTTGCACTTATCTTCTGCATTTTGCAGTCTTTGGCA
TTGACGTGGTACAGCCTTTCCTTCATACCATTTGCAAGGGATGCTGTGAAGAAGTGTTTGC
CGTGTGTCTTGCATAATTTCATGGCCAGTTTTATGAAGCTTTGGAAGGCACTATGGACAGAAG
CTGGTGGACAGTTTTGTAACATATCTTCGAAACCTCTGTCTTACAGACATGTGCCCTTTTATCT
TGCAGCAATGTGTTGCTTGTGATTGGAACATTTGAGGGTTACTTTTGAAGCAACAATACAT
TCTCGAACCTGAATGTCAGTAGCACAGGATGAGAAGTGGGTTCTGTATCTTGTGGAGTGGAA
TCTTCCTCATGTACCTGTTTCCTCTCTGGATGTTGTCCCACTGAATCCCATGAATACAAAC
CTATTCAGCAACAGCAA
AAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 201

TTGAGCGCAGGTGAGCTCCTGCGCGTTCCGGGGGCGTTCTCCAGTCAACCTCCCGCGGTTACCCGCGGCGCGC
 CCGAGGGAGTCTCCTCCAGACCTCCCTCCCGTTCGCTCCAACTAATACGGACTGAACGGATCGCTGCGAGGGT
 GGGAGGAGAAAATTAGGGGAGAAAGGACAGAGAGCAACTACCATTCCATAGCCAGATAGATTATCTTACACTG
 AACTGATCAAGTACTTTGAAAATGACTTCGAAATTTATCTTGGTGTCCCTTCATACCTGCTGCACAGTCTTTCT
 AACCACCTTTTCTCTCCAACAGACAGCAAAAGGTTCTACTAGTTCTTTTGTATGGATTCCGTTGGGATTACT
 TATATAAAGTTCCAAACGCCCATTTTCATTATATTATGAAATATGGTGTTCACGTGAAGCAAGTTACTAATGTT
 TTTATTACAAAACCTACCTTAACCATTTACTTTGGTAACCTGGCCTCTTTCGACAGAAATCATGGGATTGTTGC
 AAATGATATGTTTGATCCTATTTCGGAACAAATCTTTCTCCTTGGATCACATGAATATTTATGATTCCAAAGTTT
 GGGAGAAGCGACACCAATATGGATCACAAACCAGAGGGCAGGACATCTAGTGGTGCAGCCATGTGGCCCGGA
 ACAGATGTAAAAATACATAAGCGCTTTCCTACTCATTACATGCCTTACAATGAGTCAGTTTCATTGGGATAG
 AGTTGCCAAAATTTGTTGAATGGTTTACGTCAAAGAGCCCAATAATCTTGGTCTTCTCTATTGGGAAGACCTG
 ATGACATGGGCCACCATTTGGGACCTGACAGTCCGCTCATGGGGCCTGTCAATTCAGATATTGACAAGAAGTTA
 GGATATCTCATACAAATGCTGAAAAGGCAAAAGTTGTGGAACACTCTGAACCTAATCATCACAAAGTGATCATGG
 AATGACGCGAGTCTCTGAGGAAAGGTTAATAGAAGTTGACCACTGCTGGATAAAGACCACTATACCTGATTG
 ATCAATCTCCAGTAGCAGCCATCTTGCCAAAAGAAGGTAATTTGATGAAGTCTATGAAGCACTAACTCACGCT
 CATCCTAATCTTACTGTTTACAAAAAGAAGACGTTCCAGAAGGTGGCATTACAAATACACAGTCGAATTC
 ACCAATCATAGCAGTGGCTGATGAAGGTTGGCACATTTTACAGAATAAGTCAGATGACTTTCTGTTAGGCAACC
 ACGGTTACGATAATCGGTTAGCAGATATGCATCCAATATTTTAGGCCATGGTCCCTGCCTTCAGAAAGAAATTC
 TCAAAGAAGCCATGAATCCACAGATTTGTACCACTACTATGCCACCTCCTCAATATCACTGCCATGCCACA
 CAATGGATCATTCTGGAATGTCCAGGATCTGCTCAATTCAGCAATGCCAAGGTTGGTCCCTTATACACAGAT
 CTATACTCCTCCCTGGTAGTGTTAAACAGCAGAAATGACCAAGAGGGGTATACCCCTTATTTATAGGGGTC
 TCTCTTGGCAGCATTATAGTGATTGATTTTTTTGTAAATTTTATTAAGCATTAAATTCAGAGTCAAATACCTGC
 CTTACAAGATATGCATGCTGAAATAGCTCAACCATTATTACAAGCCTAATGTTACTTTGAAGTGGATTGGATA
 TTGAAGTGGAGATTCCATAATTATGTCAGTGTTTAAAGGTTTCAAATTTCTGGGAAACCAAGTCCAAACATCTGC
 AGAAACCATTAAGCAGTTTACATATTTAGGTATACACACACACACACACATACACACACACGACCAAAA
 ATACTTACACCTGCAAAGGAATAAAGATGTGAGAGTATGCTCCATTGTTCACTGTAGCATAGGGATAGATAAG
 ATCCTGCTTTATTTGGAGTTGGCGCAGATAATGTATATATTTAGCACTTTGCACTATGAAAGTACCTTATAT
 ATTGCACCTTTAAATTTCTCTCTGATGGGTACTTTAATTTGAAATGCACTTTATGGACAGTTATGCTTTATAAC
 TTGATTGAAATGACAACCTTTTGCACCCATGTACAGAACTGTTACGCATTGTTCAAACGAAGGAATTT
 TCTAATAATCCCGAATAATGACATAGAAATCTATCTCCATAAATGAGAGAGAAAGAGGTGATAAGTGTGA
 AAATTAATGTGATAACCTTTGAACCTTGAATTTTGGAGATGATTTCCCAACAGCAGAAATGCAACTGTGGGCAT
 TTCTTGTCTTATTTCTTCCAGAGAACGTGGTTTTTCAATTTATTTTCCCTCAAAGAGAGTCAAATACTGACAG
 ATTCTGTTCTAAATATATTGTTTCTGTCAAAATTTATGTTGATTTCCTGATGAGTCATATTACTGTGATTTC
 TAATAATGAAGACACCATGAATATACCTTTCTCTATATAGTTTCAGCAATGGCCTGAATAGAAGCAACAGGCA
 CCATCTCAGCAATGTTTTCTCTGTTTGAATTTATTGCTCCTTTGAAATTAATCACTATTAAATACATTAA
 AAATCAAATTTGATAAAAAAAAAAAAAAAAAA

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FIGURE 202

MTSKFILVSFILAALSSTFTSLQLDQOKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVHVK
QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPINRKSFSLDHMNIYDSKFWEETPIW
ITNQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKI VEWFTSKEPINLGLLY
WEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLITS DHGMTQCSEER
LIELDQYLDKDHYTLDQSPVAAILPKEGKFDEVYEALTAHPNLT VYKKEDVPERWHYKYN
SRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD
LYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPYF
IGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

Signal Peptide:

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

Somatomedin B Domain:

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

FIGURE 203

GGATTTTTGTGATCCGCGATTTCGCTCCACGGGCGGGACCTTTGTAAGTGCAGGAGGCCAG
GACAGGCCACCCCTGCGGGGCGGGAGGCAGCCGGGTGAGGGAGGTGAAGAAACCAAGACGC
AGAGAGGCCAAGCCCCTTGCTTTGGGTACACAGCCAAAGGAGGCAGAGCCAGAAGTCAAA
CCAGATCCAGAGGCAACAGGGACATGGCCACCTGGGACGAAAAGGCAGTCACCCGCAGGGCC
AAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCTTAAGGCACTTCACGGTCGTGGGAGACGA
CTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGG
AGCAGCCACCACCACACAGAGTCTCAGGCAGGAAGGCAGAGCTGCAGCCCCTGACGTTGCC
CCTGCCCCCTGGCCCCCGCACCCAGGGCCCCCCTTGACTTCAGGGGCATGTTGAGGAAACTGTT
CAGCTCCACAGGTTTCAGGTCATCATCATCTGCTTGGTGTTCTGGATGCCCTCCTGGTGC
TTGCTGAGCTCATCTGGACCTGAAGATCATCCAGCCGACAAGAATAACTATGCTGCCATG
GTATTCCTACTACATGAGCATCACCATCTTGGTCTTTTTTATGATGGAGATCATCTTTAAATT
ATTTGCTCTCCGCCTGAGTTCTTTCACCACAAGTTTGAAGATCCTGGATGCCCGTCGTGGTGG
TGGTCTCATTCATCTGACATTGTCTCCTGTTCCAGGAGCACCAGTTTGAGGCTCTGGGC
CTGCTGATTCTGCTCCGGCTGTGGCGGGTGGCCCGGATCATCAATGGGATTATCATCTCAGT
TAAGACACGTTTCAGAACGGCAACTCTTAAGGTTAAACAGATGAATGTACAATTGGCCGCCA
AGATTCAACACCTTGAGTTCAGCTGCTCTGAGAAGCCCCTGGACTGATGAGTTTGTGTATC
AACCTGTAAGGAGAAGCTCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTACTCT
CACACAGCCACCCTGAAAGTCTTGGAGTAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAG
CAGGCTGGCATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCACTGGCCAGTTA
TCACTTCAGATTACAAATCACACAGAGCATCTGCCTGTTTTCAATCACAAAGAGAACAAAACC
AAAATCTATAAGATATTCTGAAAATATGACAGAATTTGACAAATAAAGCATAAACGTGTA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 206

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKD
LDGQLDFEEFVHYLQDHEKKRLRVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEKILK
SMDKNGTMTIDWNEWDRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMW
WRHLVAGGGAGAVSRTCTAPLDRLKVLQMVASRSNNMGIVGGFTQMIREGGARSLWRGNGI
NVLKIAPESAIFMAYEQIKRLVGSDQETLRIHERLVAGSLAGIAQSSIYPMEVLKTRMAL
RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNWLQHYAVNS
ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFG
LYRGLAPNFMKVIPAVSISYVYENLKITLGVQSR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 211

CTTCTGTAGGACAGTCACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG
GAAGATGACAGCAATTATAGCAGGACCCTGCCAGGCTGTCGAAAAGATTCCGCAATAAACT
TTGCCAGTGGGAAGTACCTAGTGAAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT
TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTCCAGCACCATGAAGGGCATCCTCG
TTGCTGGTATCACTGCAGTGCTTGTTCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAT
TCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAG
CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT
TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACATTACAGCCTTCACTGTCCACGTGTCT
GCTGAAGAACACTTTTCATTTTGTAAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG
CGATGCCCTGGACCCCTCCCCTGAAGAACGTGTCCAGCAACGCAGAGTGCCCTGCTTGTATG
AATCTAATGGAACCTTCTGTCTGGGAAGCCCTGGAAATGCTATGAAGAAGAACAGTGTC
TTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTC
CAACGTCAGTAACGCCACCTGTCAGTTCCTGTCTGGTGAAAACAAGACTCTTGGAGGAGTCA
TCTTTCGAAAGTTTGAGTGTGCAAATGTAACAGCTTAACCCCCACGTCTGCACCAACCACT
TCCCACAACGTGGGCTCCAAAGCTTCCCTCTACCTCTTGGCCCTTGCCAGCCTCCTTCTCG
GGGACTGCTGCCCTGAGGTCTTGGGGCTGCACTTTGCCCAGCACCCCATTTCTGCTTCTCTG
AGGTCCAGAGCACCCCTGCGGTGCTGACACCCTCTTCCCTGCTCTGCCCCGTTTAACTGC
CCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTTCTTCATTATTA
AAGCACTGGTTCATTCACTGCCAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 213

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCA
GGGCTTGCCCTCACTGGCCACCCCTCCCAACCCCAAGAGCCCAGCCCCATGGTCCTCCCGCGCCG
GCGCGCTGCTGTGGGTCTGCTGCTGAATCTGGGTCCCCGGGCGGCGGGGGCCCAAGGCCTG
ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGCCCCATGACCCGCGAG
CTACCCGAGCACC GCCCGGACTGGTCTTCCCCGGAAGACAAGGATAATCCTAGAGGACGAGA
ATGATGCCATGGCCGACGCCGACCGCTGGCTGGACCAGCGCTGCCGAGCTCTTGCCCGCC
ACGGTGTCACCGGCTTTAGCCGGTCGTCGCCATTAAACGAGGAGGATGGGTCTTCAGAAGA
GGGGGTGTGATTAATGCCGGAAGGATAGCACCAGCAGAGAGCTTCCCAGTGCGACTCCCCA
ATACAGCGGGGAGTTCCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG
ACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC
CCTGAGCCAGTGGTCCACACCTGGGTCTACCCCGAGCCGGTGCCCGTCACCTCACCACAG
CCATGCCATCTCCTGAGGATCTGCGGCTGGTGTGATGCCCTGGGGCCCGTGCCACTGCCAC
TGCAAGTCGGGCACCATGAGCCGAGCCGGTCTGGGAAGCTGCACGGCCTTTCGGGCGCCT
TCGAGTTGGGGCGCTGAGCCAGCTCCGCACGGAGCACAAGCCTTGCACCTATCAACAATGTC
CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT
GCCTCTCAGAGCACCACCAGTACCAGGACCACCCTACCCCTTCCCCACCATCCACCTCAG
AAGCAGTCCCAGCCTGCCACCCGCCAGCCCTGCCAGCCCTGGCTTTTGGAAACGGGTCA
GGATTGGCCTGGAGGATATTGGAATAGCCTCTCTTCAGTGTTCACAGAGATGCAACCAATA
GACAGAAACCAGAGGTAATGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCT
CTTGCCCTTTCAATCCTAGCACCCACTAGATATTTTAGTACAGAAAAACAAACTGGAAAA
CACAA

CCCGGGTCGACCCACGCGTCCGGGGAGAAAGCA**ATG**CGCGCGCTGGCGGCGCGTTGGTCCGCGTACGTGGGCA
CGCGCGCTGGCGAGCGGCTCCCGAGGCGACCGTGAAGCGGTTACCGGACGTGGTACTGCGTGGAGAGCA
GAACCTGCTCTGGGGCGCTGTGAATCACTCCGCTCCGCGACGCAATCTACATGCTCTAGAGCGCTGGACCT
CTGGGACGAGCTGTAAATATGAGTGTATGTGTGGGTCAACGCTGGGGCTCTACTCCAGGAAGGTCAAAAGTGCCCT
CAGTTCACATGSCAAGTGGCCCTCTCCCGGTTCTCTGTTCTTTCAAGAGCGCGCTACGCGCTGGCCCTGTTTCT
CAATGGCCCTGGCCAGCCTGGTGTATGCTCTGCGGCTACCGCACCTTCTGTGCCAGGCTCTCTCCCCCTGTATACCAC
CTCTGTGTGCCCTTCGCGTGGGTGTCCCTCAATGCACTGGTTTGGTGCACAGTCTTCCACACAGGGGACACTGA
CTCAGACAGAAAGATGGACATCTCTGTGCCCTCACTGTATCTACACTCAATCACTACCTGTGCTGGTCAAGAC
CTGGGGCTCGACGACCAAGTGTGGTCACTGGCTCTCCGGGCTCTCTCGCTGTCTCATGCTACGCTGCACGTCT
CTCTACTGAGCCTCATCGCTTCGACTATGGCTACAACTGGTGCCCAAGTGGCTATGGCTACCTGTCAAGTG
GTGTGGTGGCTGGCTGTGTGCTGTGGAACACGCGGCGCTGCCCTACGTCGCGCAAGTGCCTGGTGGTGGTGTCT
GTGCTGTGCGAGGGGTGTGCCCTGTGCGAGTGTGTGACTCTCCACCGCCTCTCTGGGTCTGGATGCCATGCCA
TGTGGACATCAGCACCATCCCTGTCCAGCTCCCTCTTTTTCAGCTTTCTGGAAGATGACAGCGTCTAACCTGTG
AAGGATCAGGAGCAAACTCAAAGCTGAG**CGA**AGACCTTGAGGACGAGTCTGCCGACGAGTGGGATGGGATCTGCCCC
GCCCTGCTGGCTCCCTTCTCCCTCCAACTCTGAGATGATTTTCTCTTTCACTTCTTGAACCTGGACATGGA
AGGATGTGGGCCCAAGATCATGTGCCAGCCACCCCTCTGTGGCCCTCACCAGCCTTGAGGTCTGTTCTTAGG
AAGGCTCTCCAGCATCTGGGACTCGAGAGTGGGCGAGCCCTCTACCTCTGGAGCTGAATCGGGGTGSAATCTGA
GTGTGTTCTTACGCTCTACCGGAGGACAGCTGCTCTTTCTCCCCACAGGCTCTCCCCCATCCCCAGCTG
CTGTGCTGGGTCTCGAAGCCCTCTGTCTACTCTACCTGGGAGACAGGGAACAGGCCCTTAGGATCAAGGGGGTCCC
CTTCTCTTACCAACCCACCCCTCCGAGGACACCATAGTGGTGCTGTGATGCTGTTCTTCTTGGCCAGCCAA
GGTTACGCGCGATTTCTCCCATGGGATCTTGAGGGACACCTGCTGGGATTGGAAGGAGTTTCCACCTGACC
GTTGCCCTAGCCAGGTTTCCAGGAGGCTCACCATACTCCCTTCCGGGCCAGGGTCTCAGCAAGGCCAGGGCA
AGGATCCTGTGCTGTCTGTGGTGGAGGCTGCCACCGTGTGTGCGGAGTGTGGGCCAGGCTGAGTGCATAGG
TGACAGGGCCGCTGACATGGGCTGGGTGTGTGTGAGCTCAGGCTAGGTGGCGCAGTGTGGAGACGGGTGTGTG
CGGGAGAAAGGTTGGCTTCAAAGTGTGTGTGTGTCAGAGGCTGGGTGTGTGTAAGCTGGGTTAGGGAGACGTGTG
TGCGGATCTGTGGTGGGACTGTGATAGATGAGTGACTGCGCGGTGAATGTGTCACAGCTTGAGAGCTTGTGAGCAGAT
GAGGGAATCCTGTACCATCAATAATCACTTGTGGAGCGCGAGCTGTGCCAAGACGCGCTTGGGCGACGACG
CAGGAGCTCTCCATGGCCAGGCTGCCCTGTGTGCATGTTCCTCTCTGTTGGCCCTTTGGCCGCGCTCTGCTCAAA
CTCAGAGGTCGCCCAACAAGTGCCTCCGACGAAGCGCCCTCGAGGACGAGGAAATGGGATGCG
TGGGCTCTCTCCATCTCTCTCTCTCTGCTTCGATCGATGGTGGCTCTCCCTCCAAACCTCCATCTCCCT
GCTGCGAGCCCGTTTGGCATGACTGATTTTGGGAGGAGGAGAGGGGCGCTTTGAGGAGAGAGGGGAGAGGCT
TATGGCTGGGTGTGGTTTCTCCCTTCCGAGGAGTCTACTGTCTCCAGGTTGCCCCAGGCGACGAGGCGCT
ACACTATGCTCTGCGCCTCGTAAGAGGTGACCCCTGCCATTTACACGACGCTGGCATGTCTCTGCCCCACAGG
AATAGATGGAGGGAGCTCGAAGAACTTTCATCCCAAGGCACTCTCGTGGTTGAAGCAAGCTGGATTTTGG
CTCTGCCCTGACCCCTGTGCCCTCTTGGAGGAGGGGAGCTATGCTAGGACTCCAACCTCAGGGACTCGGGTG
GCTCGGCTAGCTTCTTTTGATATCGAAACTTTTAAGTGGGAGGGTGGCAAGGGATGTGCTTAATAAATCAA
TTCCAGACTCTAAAAAATAAAAAAATAA

FIGURE 216

MAGLAARLVLLAGAAALASGSQGDREFVYRDCVLQCEEQNCSSGGALNHFRSRQPIYMSLAGW
TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWPFSSRFLFFQEPASAVASFLNGLASLVMLCR
YRTFVPASSPMYHTCVAFWVSLNAWFSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVR
TVGLQHPAVVSAFRALLLLMLTVHVSYSLSLIRFDYGYNLVANVAIGLVNVVWWLAWCLWNQR
RLPHVRKCVVVLLIQGLSLELLDFPPLFWVLDAHAIWHISTIPVHVLFSSFLEDDSLYLL
KESEDKFKLD

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

[illegible]

MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPEKSSSTKETERKETKAEEL
DAEVLEVHFHPTHEWQALPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTN
TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV
RLINKFNSSSSSLEEKIAALFDLEYVYVHQMDNAQDLLSFGGLQVVINGLNSTEPLVKEYAAF
VLGAAFSSNPVKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL
GGLQVLRTLVQEKGEVLAVRVVTLTYDLVTEKMFEEEEAELTQEMSPEKLQQYRQVHLLPG
LWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLAS
LELQDGEDEGYFQELLSVNSLLKELR

Signal peptide:

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

FIGURE 219

TTCGGCTTCCGTAGAGGAAGTGGCGCGGACCTTCATTGTTGGGGTTTCGGTTCCCCCCTTCCC
 CTTCCCCGGGGTCTGGGGGTGACATTGCACCGCGCCCCCTCGTGGGGTTCGCGTTGCCACCCCCA
 CGCGGACTCCCCAGCTGGCGCGCCCCCTCCCATTTGCTGTCTGGTCAGGCCCCCACCCTTCC
 TTCCACCTGACCAGCC**ATG**GGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTGCGCTTCGGC
 CCGGCCTTCGCGCTTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCTCGGT
 CGCAGGGGCATTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGG
 TCCATGTGACCGACCGGTGATGATGCCCCGGCTCCAGTACGGCTCCTGATTTTTGGTGTCTGCT
 GTCTCTGCTCTTCTACAGGAGGTGTTCCGCTTTGCTACTACAAGCTGCTTAAGAAGGCAGA
 TGAAGGGTTAGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCT
 ATGTTTCTGGTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCT
 GATGCACCTGGGCCAGGTGTGGTTGGGATCCATGGAGACTCACCTATTACTTCTGACTTC
 AGCCTTTCTGACAGCAGCCATTATCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATG
 CCTGTGAGAGGAGACGGTACTGGGCTTTGGGCCTGGTGGTGGGAGTCACCTACTGACATCG
 GGACTGACATTCTGAACCCCTGGTATGAGGCCAGCCTGCTGCCCATCTATGCAGTCACTGT
 TTCCATGGGGCTCTGGGCCTTCATCACAGCTGGAGGGTCCCTCCGAAGTATTCAGCGCAGCC
 TCTGTGTAAAG**ACTG**ACTACCTGGACTGATCGCCTGACAGATCCCACCTGCCTGTCCACTG
 CCCATGACTGAGCCAGCCCCAGCCCGGGTCCATTGCCACATTCCTGTGCTCCTTCTCGTC
 GGCTACCCCACTACCTCCAGGGTTTGTCTTTGTCTTTTGTGACCGTTAGTCTCTAAGCTT
 TACCAGGAGCAGCCTGGGTTCAGCCAGTCAGTGACTGGTGGGTTTGAATCTGCACTTATCCC
 CACCACCTGGGGACCCCTTGTGTGTCCAGGACTCCCCCTGTGTGCTGCTGCTCTCAC
 CCTGCCCAAGACTCACCTCCCTTCCCTCTGCAGGCCAGCGCAGGAGGACAGTCGGGTGAT
 GGTGTATTCTGCCCTGCGCATCCCACCCGAGGACTGAGGGAACCTAGGGGGGACCCCTGGGC
 CTGGGGTGCCCTCCTGATGTCTCGCCCTGTATTTCTCCATCTCCAGTTCTGGACAGTGCAG
 GTTGCCAAAGAAAGGACCTAGTTTTCAGTACTCCCTCAAGACTGGACATCTTGGTCTTTTTCTC
 AGGCCTGAGGGGGAACCATTTTTGGTGTGATAAATACCCTAAACTGCCTTTTTTCTTTTTT
 GAGGTGGGGGGAGGGAGGAGGTATATTGGAACCTCTTCAACCTCCTTGGGCTATATTTTCTC
 TCCTCGAGTTGCTCCTCATGGCTGGGCTCATTTCCGGTCCCTTTCTCCTTGGTCCCAGACCTT
 GGGGGAAGGAAGGAAGTGCATGTTTGGGAACTGGCATTACTGGAACATAATGGTTTTAACCT
 CCTTAACCACCAGCATCCCTCCTCTCCCCAAGGTGAAGTGGAGGGTGTGTGGTGAGCTGGC
 CACTCCAGAGCTGCACTGCCACTGGAGGAGTCAGACTACCATGACATCGTAGGGAAGGAGGG
 GAGATTTTTTTGTAGTTTTTAATTGGGGTGTGGGAGGGGCGGGGAGGTTTTCTATAAACTGT
 ATCATTTTCTGCTGAGGGTGGAGTGTCCCATCCTTTTAAATCAAGGTGATTGTGATTTTGACT
 AATAAAAAAGAAATTTTAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 227

ATGGTCAACGACCGGTGGAAGACCATGGGCGGCGCTGCCAACTTGAGGACCGGCCGCGCGCA
 CAAGCCGACGCGGCCGAGCTGCGGCTACGTGCTGTGCACCGTGTCTGCTGGCCCTGGCTGTGC
 TGCTGGCTGTAGTGTACCGGTCGCGTGCTCTTCTGAACACCGCCAGCCGCGGCGCAG
 GCGCCCCACCTGTCTGTAGCACTGGGCTGCCAGCGCCAACAGCGCCCTGGTCACTGTGGA
 AAGGGCGGACAGCTCGCACCTCAGCATCCTCATTGACCCGCGCTGCCCGGACCTCACCGACA
 GCTTCGCACGCGCTGGAGAGCGCCAGGCGCTCGGTGCTGCAGGCGCTGACAGAGCACCGGCC
 CAGCCACGGCTGGTGGGCGACAGGAGCAGGAGCTGCTGGACACGCTGGCCGACAGGCTGCC
 CCGGCTGCTGGCCCCAGCCTCAGAGCTGCAGACGGAGTGATGGGGCTGCGGAAGGGGCGATG
 GCACGCTGGGCCAGGGCCTCAGCGCCTGCAGAGTGAGCAGGGCGCGCTCATCCAGCTTCTC
 TCTGAGAGCCAGGGCCACATGGCTCACCTGGTGAACCTCCGTAGCGACATCCTGGATGCCCT
 GCAGAGGGACCGGGGCTGGGCCGGCCCCGCAACAAGGCCGACCTTCAGAGAGCGCTGCC
 GGGGAACCCGGCCCCGGGGCTGTGCCACTGGCTCCGGCCCCGAGACTGTCTGGACGTCCTC
 CTAAGCGGACAGCAGGACGATGGGCTCTACTGTCTTTCCACCCACTACCCGGCCGGCTT
 CCAGGTGTACTGTGACATGCGCACGGACGGCGCGCGCTGGACGGTGTTCAGCGCCGGGAGG
 ACGGCTCCGTGAACCTTCTCCGGGGCTGGGACGCGTACCGAGACGGCTTGGCAGGCTCAC
 GGGGAGCACTGGCTAGGGCTCAAGAGGATCCACGCCCTGACCACACAGGCTGCCTACAGCT
 GCACGTGGACTGGAGACTTTGAGAAATGGCACGGCCTATGCCCGTACGGGAGCTTCGGCG
 TGGGCTTGTCTCCTGGACCTGAGGAAGACGGGTACCCGCTCACCGTGGCTGACTATTCC
 GGCATGACGGCGACTCCTCCTGAAGCACAGCGGATGAGGTTCAACACCAAGGACCTGGA
 CAGCGACCATTCAGAAACAACTGTGCCGCTTCTACCGCGGTGCTGGTGGTACCGCACT
 GCCACAGCTCCAACCTCAATGGGCGAGTACCTGCGCGGTGCGCACGCTCCTATGCCGACGGC
 GTGGAGTGGTCTCTGGACCGGCTGGCAGTACTCACTCAAGTTCTCTGAGATGAAGATCCG
 GCGGTCGGGGAGGACCGCTAGACTGGTGCACCTTGTCTTGGCCCTGCTGGTCCCTGTGCG
 CCCATCCCCGACCCACCTCACTCTTTCGTGAATGTTCTCCACCCACCTGTGCCTGGCGGAC
 CCACTCTCCAGTAGGGAGGGGCGGGCCATCCTGACACGAGCTCCTGGGCGGTTGAAGT
 CACACATCGCTTCTGCGGCTCCCCACCCCTCCATTTGGCAGCTCACTGATCTCTTGCCCTC
 TGCTGATGGGGGCTGGCAAACCTTGACGACCCCAACTCCTGCCGCCCACTGTGACTCCGG
 TGCTGTTTGGCTCCCTGGCCAGGATGGTGGAGTCTGCCCAAGCACCTCTGCCCTGCC
 GGCCAAATACCCGGCATTATGGGGACAGAGAGCAGGGGGCAGACAGCACCCCTGGAGTCCCTC
 CTAGCAGATCGTGGGAATGTCAAGTCTCTCTGAGGTCAAGTCTGAGGCCAGTATCTCCAG
 CCTCCCAATGCCAACCCACCCCGTTTCCCTGGTGCCACAGAAACCCACCTCTCCCCAA
 GGGCTCAGCTGGCTGTGGGCTGGGTGGCCCCATCCTACAGGCCCTGAGGTCAAGATGGG
 GAGTGTCTGCTTTGGGGACCCACGCTCCAAGGCTGAGACGATTCCTGGAGGCCACCCAC
 CCTGTGCCCGGGCAGGCCTGGGCTGTCAGTCTCTTACCTGCTGTGCCACCTGCTCTCTG
 TCTCAAATGAGGCCCAACCCATCCCCACCCAGCTCCCGGCGTCCCTCACTGGGGCAGC
 CGGGCTGCCATCCCAATTTCTCTGCTCTGGAAGTGGGTGGGGCCTGACCGTGGGGCT
 GGACTGCGCTAATGGGAAGCTCTTGTTTTCTGGGCTGGGGCTAGGCGGGCTGGGATGAG
 GCTTGTACACCCCCACCACCAATTTCCAGGGACTCCAGGGTCTGAGGCTCCAGGAGG
 GCCTTGGGGGTGATGACCCTTCCCTGAGGTGGCTGTCTCCATGAGGAGGCCAACCTTGGC
 ATTGACCGTGGCCACCTGGACCCAGGCCAGGCCCGCGGAGTGGTCAAGGGACAGGGA
 CCACCTCACCGGGCAATATGGGGTGGGGGGACTGGGGCACAGACAGGCCACCCACCTGGACA
 CTTTCTTGTGTAATCTCCCAACCCAGCACGCTGTATCCCCACTCTTGTGTGCACACA
 TGAGAGGTTGAGACCCGACGGCTCCAGGACAGCACGACCAAGGGCAGGGCTGGAGCCGGG
 TCTCAGCTGTCTGCTCAGACGCTGAGACCCGCGTGCCTTACGTACGACGGCCAGATGACGG
 CGGCTTTTCAAGGCTCTCTGATGGGGGCTCCGAAAGGGCTGGAGTCAAGCTTGGGGAGCT
 GCCTAGCAGCTCTCTCGGCGAGGAGGGAGGTGGCTTCTCTCAAGGACACCCGATGGCA
 GGTGCTAGGGGCTGTGGGTTCCGTTCTCCCTTCCCTCCCACTGAAGTTTGTGCTTAA
 AACAAATAATTTGACTTGGCACCCTGGGGGTTGGTGGGAGAGGCCGTGTGACCTGGCTCTC
 TGTCCAGTGCCACCAAGGTCATCCACATGCGCAG

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FIGURE 228

MVNDRWKTMGGAAQLEDRPRDKPQRPSCGYVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGT
APPPVVSTGAASANSALVTVERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALTEHQA
QPRLVGDQEQELLDTLADQLPRLARASELQTECMGLRKGHGTLGQGLSALQSEQGRLIQLL
SESQGHMAHLVNSVSDILDALQDRGLGRPRNKADLQAPARGTRPRGCATGSRPRDCLDVL
LSGQQDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTVFQRREDGSVNFFRGWDAYRDGFGRLT
GEHWLGLKRIHALTTQAAYELHVDLEDFENGTAAYARYGSFGVGLFSVDPEEDGYPLTVADYS
GTAGDSLLKHSGMRFTTKDRSDSHSENNCAAFYRGAWWYRNCHTSNLNGQYLRGAHASADG
VEWSSWTGWQYSLKFSEMIRPVREDR

GCAGTCACAGAGACTTCCCCTGCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTACTGCTT
TGCTTCTGAACTAGCTCACAGTAGCCCCGGCGCCAGGGCAATCCGACCACATTTCACTCT
CACCGCTGTAGGAATCCAGATGAGGCCAAGTACAGCAGCAGAGGGACATGCTGGATGATG
ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTGGCATCCAGAGCCC
CGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCTTGCTGAC
TTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTTCAGTACTACC
AGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATACGTCC
CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGAGGAAGTCTGCAGCATGTGGC
TGAAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAG
AACAAATGGAATGGCATGGAGACAATTGCTACCACTTCTATAAAGACAGCAAAAGTTGGGAG
GACTGTAAATATTTCTGCCTTAGTGAAAACCTCTACCATGCTGAAGATAAAACAACAAGAAG
CCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTT
TGCGCCCTGACAGTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTTCACTTCTGAACTG
TTCCATATTATAATAGATGTCACCAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGG
GATGATCTTCTCAAAGGACTGCAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAA
TGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGATTGCCC
CTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACAT
TGGGAAATGGAACATAATCAGGAAGACTATCTCTCTGACTAGTACAAATAGGGTTCTCGTG
TTTCTGTTCAGGATCACCAGCATTCTCTGAGCTTGGGTTTATGCACGTATTTAACAGTACA
AGAAGTCTTATTACATGCCACCAACCAACCTCAGAAACCATAATGTATCTGCCTTCTTG
GCTTAGAGATAACTTTTAGCTCTCTTTCTTCTCAATGTCTAATATCACCTCCCTGTTTTTCAT
GTCTTCCCTTACACTTGGTGAATAAGAAACTTTTTGAAGTAGAGGAAATACATTGAGGTAAC
ATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACTTCCAGATTGTACC
AGCAAAATACACAAGGAATTCTTTTGTGTTGTTTCAGTTTCATACTAGTCCCTTCCCAATCCAT
CAGTAAAGACCCCATCTGCCTTGTCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAG
AATCTCAAATCTCAATGCCTTATAAGCATTCCTTCTGTGTCATTAAAGACTCTGATAATTG
TCTCCCTCCATAGGAATTTCTCCAGGAAAGAAATATATCCCATCTCCGTTTCATATCAG
AACTACCGTCCCCGATATTCCCTTCAGAGAGATTAAGACAGCAAAAAAGTGAGCCTCTTCA
TCTGCACCTGTAATAGTTTCAGTTCCTATTTTCTTCCATTGACCATATTTATACCTTTCAG
GTACTGAAGATTTAATAATAATAAATGTAAATACTGTGAAAAA

AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTCCGCATCCAG
AGCCCCGGCGCACAGAGCACAGGGNTCCTTTTTCAACGTGGCGACCAAGTGGCCCTGACCCTG
CTGACTTTGTGCTTGGTGTCTGATAGGGCTGGCAGCCCTGGGGCTTTGTTTTTTCAGTA
CTACCAGCTCTCAAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATA
CGTCCCAAGAGTTGCAATTTNTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTNTGCAGCAT
GTGGCTGAAAAACTCTGTCTGAGCTGTATAACAAAGCTGGAGGAACCTTTGAAGGAGGGCAA
AGTNTCCTCATNTACTATACACACCACTTCCC

[illegible]

FIGURE 233

MRASLLLSVLRPAGPVAVGISLGFTLSLLSVTWVEEPCGPGPPQPGDSELPPRGNTNAARRP
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAACKAVRTRYISTELGIRQLLVAVL
TSQTTLPTLGVAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHHLHLALRHLL
QHGDDEFWFFLVPDTTYTEAHGLARLTGHLSLASAAHLYLGRPQDFIGGEPTPGRYCHGGFG
VLLSRMLLQQLRPHLEGCRNDIVSARPDEWLGRCIL DATGVGCTGDHEGVHYSHLELSPGEP
VQEGDPHFRSALTAPVRDPVHMYQLHKAFARAELEPTYQEIQELQWEIQNTSHLAVDGDRA
AAWPVGIPAPSRPASRFEVLRWDYFTEQHAFSCADGSPRCPLRGADRADVADVLGTAEELN
RRYHPALRLQKQQLVNGYRRFDPARGMEYTLDLQLEALTPQGGRRPLTRRVQLLRPLSRVEI
LPVPYVTEASRLTVLLPLAAAERDLAPGFLEAFATAALEPGDAAAALTLLLLYEPRQAQRVA
HADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPRLRLMDLLSKKHPLDTLFLLAGPDTVL
TPDFLNRCRMHAISGWQAFFPMHFQAFHPGVAPPQGGPPPELGRDTGRFDRQAASEACFYNS
DYVAARGRLAAASEQEEELLES LDVYELFLHFSSLHVLR AVEPAL LQRYRAQTCSARLSEDL
YHRCLQSVLEGLGSRTQLAMLLFEQE QGNST

FIGURE 234

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT
 TGGCAAGCGCTGGCCACCTCCCCACACCCCTTGCGAACGCTCCCCTAGTGGAGAAAAGGAGT
 AGCTATTAGCCAATTCTGGCAGGGCCCGCTTTTGTAGAGCTTGATTTCTTTGAAGATGAAAG
 ACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGGAACCGGGGCGATTGGCTGGGAA
 CTGTATCCACCCAAATGTCACCGATTCTTCTCTATGCAGGAAATGAGCAGACCCATCAATAA
 GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACTGGAGGCAAAG
 AGGGTTGCTCAACGCCCCGCCTCATTTGAAAACCAAATCAGATCTGGGACCTATATAGCGTG
 GCGGAGGCGGGGCGATGATTGTGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTTCT
 TTTCCCGCCCCCTGAGACCTGCAGCACCATCTGTCTATGGCGGCTGGGCTGTTGGTTTGAGC
 GCTCGCCGTCTTTTGGCGGCAGCGCGACGCGAGGGCTCCCGGCCGCGCCGCTCCGCTGGGA
 ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGGAAGCGCCCCCAGAAC
 CGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAACCTGTATGAGAAGAACCA
 GACTCCCATGGTTATGACAAGGACCCCGTTTGGACGTCTGGAACATGCGACTTGTCTTCTT
 CTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACCTTTGTGGCCTATCTGCCTGACTACA
 GGATGAAAGAGTGGTCCCGCCGGAAGCTGAGAGGCTTGTGAAATACCGAGAGGCCAATGGC
 CTTCCTCATGGAATCCAACCTGCTTCGACCCAGCAAGATCCAGCTGCCAGAGGATGAGTG
ACCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATTCTGAC
 CTCTTCTCAGAGCACCTAATTAAGGGGCTGAAAGTCTGAA

FIGURE 235

MAAGLFLGSARRLLAAATRG LPAARVRWESSFSRTVVAPS AVAGKRPEPTTPWQEDPEPE
DENLYEKNPDSHGYDKPVL DVNMRLVFFGVSIILVLGSTF VAYLPDYRMKEWSRREAER
LVKYREANGLPIMESNCFDPSKIQLPEDE

FIGURE 236

GCGGCGGCT**ATG**CCGCTTGCTCTGCTCGTCCGTTGCTCTCTGGGGCCCGCGGCTGGTGCCTTGCAGAACCCCCACGCGACAGCTTGCGGGAGGAACCTGTGCATACCCCGCTGCCTTCCGGGACGTAGCCGACATTCAGTTCCGTCAGCGCTGGGATTCGGAGCTTCAGCGGGAAGGAGTGTCCCATTCACAGGCTCTTTCCAAAGCCCTTGGGGCAGCTGATCTCCAAGTATTCTCTACGGGAGCTGCACTGTCAACAAAGGCTTTTGGAGGACCCGATACCTGGGGGCCACCTTCTCTGAGGCCCATCAGGTGCAGAGCTGTGGGTTCAGGTTCCAAAGACATGTCACTGATGTGGATAAATCTTTGGAAGAGAGCTCAGTAATGTCTCTAGGATCTTCTTGCCGCTCTCAACTTCATTCGACTCCCAACACAGCTGACCTGCCATGCCCTCCTTCAAACCCGCTGGGTCTGGCCAACTGACACTGACCACTACTTTCTAGCTATGCTGTGCTGCCCGGGAGGTTGCTGCACCGAAACCTCACCCTCGAAGAGAGCTTTGCCCTGTAGTTTCCAAGCAGGCCCTCTGTGCTGCTGAAGGCAGATCGCTTGTTCACACACAGGCTACCACTCCCAAGCCAGTGCATATCCGCCCTGTCTGTCAGAAATCAGCGTGTACTAGCATCTCTGGGAGCTGAGGCAGACCTGTTCAGTTGTATTTGATGCTCATTATCAGGGGAGGAGAAAGAACTGGTCCCTCTCCGGATGTCTCCGAACCTCACGGA GCCCTGCCCCCTGGCTTCAGAGAGCCGAGTCTATGTGGACATCACCCCTACAACCAGGACACAGACAGATTAGAGGTGCACCCACCCCGACATACATCAGCAGCTACCTCATGGAGCTCGGAAGACCTTAGGCATCTAGCTATGACTTGCTTGACCCGCGATGATCAACAACTCTGAAACCTCAACATCCAGCTCAAGTGAAGAGACCCCAAGAGAATGAGGCCCCCCCAGTGCCTCTCTGATGCCAGCCGTACGTGAGTGGCTATGGGCTGCGAAGGGGAGCTGAGCACATGCTGTGATAACACCCACCATACCGGCCCTTCCCGTGCTGCTGCTGGACACCGTACCTGTGATCTGCGGCTGTATGTGCACACCTCACCATCACCTCCCAAGGGCAAGGAGAACAAACCAAGTTACATCCACTAACCGCTGCCCGAGGACCGGCTGCAACCCCACTCTCGGAGATGCTGATTACGTGCCGCCCAACTCAGTACCAAGGTTTCCATCCAGTTTGAAGCGGCGCTGCTGAAGTGACCCAGTAGTACCGGCAGATCTCAGCATGCCATAGGCTTCTATGTGACCCCATCTGTCTCTCAGCGCCCTTGTGCCCA GCATGGTAGACGCAAGCCAGTGAGCTGGGAAGAGAGTCCCCCTCTCAACAGCCTGTCTCCCA GTCTCTGATGGCTCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAATCCGCCGACACCGGACTCAGCATGCCATCAACGCTGATCTGCCTCAGTGCAGCTGTGGTGGCCGTGTGCTACGGGCTCCTTCTACAATCTCCTCACCCGAACCTTCCACATCAGGAGGCCGCCGACAGGTGGCTGGCCAAAGCGGCTGGCCAACTTATCCGGCGCGCCGAGGTGTCCCCCACT**TGA**TCTGCCCTTTTCAGCAGCTGCAGCTGCCCTTTCTCTCTGGGAGGGGAGGCCAAGGCTGTTTCTGCCACTTGTCTCTCCTCAGAGTTGGCTTTTGAACCAAAGTGCCTTGACCAGCTCAGGCGCTACAGCTGTGTGTCAGTAGCAGGACCGACGCAAGTGTGCCATTTGAATTTGAATTTAATCTAGAAATCATTTCTCACTGTAGTGGCCATCTATATTGAGGTGCTCAATAAGCAAAAGTGGTCSGTGGCTGCTGTATTGGACGACAGACAGAAAGATTTCCATCACCAAGAAAGGTCGGCTGGCAGCACTGCCCAAGGTGATGGGGGTGTGCTACACAGTGTATGTCACTGTGTAGTGGA

FIGURE 238

MPLALLVLLLLGPGGWCLAEPPRDSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHY
RLFPKALGQLISKYSLRELHLSFTQGFWRTRYWGPPFLQAPSGAELWVWFQDVTVDVDSWK
ELSNVLSGIFCASLNFIDSTNTVTPTASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWK
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCARNARCTSSISWELRQTLVVFDFAFITG
QGKKDWSLFRMFSRTLTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTTYQDVILGTRKT
YAIYDLDTAMINNSRNLNIQLKWKRPPENEAPPVPFLHAQRYVSGYGLQKELSTLLYNTH
PYRAFPVLLLDTPWYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANS
VTKVSIQFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSD
GSNYFVRLYTEPLLVLNLTPTDFSMYPNVICLTCTVVAVCYGSFYNNLLTRTFHIEEPRTGGLA
KRLANLIRRARGVPPL

FIGURE 239

CAACATGGGGTCCAGCAGCTTCTTGCTCCTCATGGTGTCTCTCGTTCTTGTGACCCCTGGTGG
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTTGCCCAGCTGACAACGTACGC
TGCTTCAAGTCCGATCCTCCCCAGTGTACACAGACCAGGACTGTCTGGGGGAAAGGAAGTG
TTGTTACCTGCACTGTGGCTTCAAGTGTGTGATTCTGTGAAGGAAGTGAAGAAGGAGGAA
ACAAGGATGAAGATGTGTCAAGGCCATACCTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC
TCCTCCTCTACCAGGTGTCTCAGAAATGATGCTGGGTCTTTCTACCTCTGGGGGTCACTC
TCACTTGGCACCTGCCCCTGAGGGTCTGAGACTTGGAATATGGAAGAAGCAATACCCAACC
CCACCAAAGAAAACCTGAGCTTGAAGTCCTTTTCCCCAAAAGAGGGAAGAGTCACAAAAAG
TCCAGACCCAGGGACGGTACTTTCCCTCTCTACCTGGTGCTCCTCCCTAATGCTCATGAAT
GGACCCCTCATGAATGAAACCAAGTGCCTTATAAGAGACCCCAAAGAGCTGCCTTGCCCTTC
TGCAATGTGTGATCACAGCTAGAAGGCACTGTCAGAGAAGAGAACTGGTCTCACCAGATG
CTGAATCTGCTGGTGCCTTGATCTTGGAAGTCCCAGCCTCTAGAAGTGAAGAAATAAATAT
TTGCTGTTTATAATCCAA

000000-111111

amino acids 49-63

FIGURE 241

AAACCTCAGCACTTGCCGGAGTGGCTCATTGTTAAGACAAAGGGTGTGCACCTTCTGGCCAGG
 AAACCTGAGCGGTGAGACTCCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACTTCC
 TCTAGAACCAGCCACCACCACCAATGAGGTCTGCTGTGGAGATGCAGGCACCTGAGCCAAGG
 CGTCCAGTGGTCTGTGCTTCTGGTGTCTGCTGGTCTCTTTTCTCTTCGCGCTTGCCCTTTT
 TTAAGGAGCCTCAAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAAGAAAGGTCT
 CTACAGTCCCTGGCAAAGCCTAAGTCCCAGGCACCCACAAGGGCGAGGAGGACAACCATCTA
 TGCAGAGCCAGCGCCAGAGAACAAATGCCCTCAACACACAAACCCAGCCCAAGGCCACACCA
 CCGGAGACAGAGGAAAGGAGGCCAACAGGCACCGCCGAGGAGCAGGACAAGGTGCCCCAC
 ACAGCACAGAGGGGAGCATGGAAGAGCCCCAGAAAAGAGAAAACCATGGTGAACACACTGTC
 ACCCAGAGGGCAAGATGCAGGGATGGCCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCC
 AGGACACAAAGACGCCCAAGGAAATGGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGACG
 GTGTCAGAGAAGCACCAGGGCAAAGCGGCAACCACAGCCAAGACGCTCATTCCAAAAGTCA
 GCACAGAAATGTGTGCTCCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCA
 CAGCAGTCATCCCACCTAAGGAGAAACCTCAGGCCACCCACCCCTGCCCTTCCAG
 AGCCCCACGACGCAGAGAAAACCAAAGACTGAAGGCCGCCAACTTCAAATCTGAGCCTCGGTG
 GGATTTTGAGGAAAAATACAGCTTCGAAATAGGAGGCTTCAGACGACTTGCCCTGACTCTG
 TGAAGATCAAAGCCTCCAAGTCGCTGTGGTCCAGAACTCTTTCTGCCAACCTCACTCTC
 TTCTTGGACTCCAGACACTTCAACCAGAGTGAGTGGGACCCCTGGAACTTTGCACCACC
 CTTTGGCTTCATGGAGCTCAACTACTCCTTGGTGCAGAAGGTCGTGACACGCTTCCCTCCAG
 TGCCCCAGCAGCAGCTGCTCCTGGCCAGCCTCCCCGCTGGGAGCCTCCGTTGCATCACCTGT
 GCCGTGGTGGGCAACGGGGGCATCCTGAACAACCTCCACATGGGCCAGGAGATAGACAGTCA
 CGACTACGTGTTCCGATTGAGCGGAGCTCTCATTAAAGGCTACGAACAGGATGTGGGGACTC
 GGACATCCTTCTACGGCTTTACCGCCTTCTCCCTGACCCAGTCACCTCTATATTGGGCAAT
 CGGGGTTTCAAGAACGTGCCTCTTGGGAAGGACGTCCTGCTTGCACCTTCTGGAAGGCAC
 CCGGGACTATGAGTGGCTGGAAGCACTGCTTATGAATCAGACGGTGATGTCAAAAAACCTTT
 TCTGGTTCAAGGCACAGACCCAGGAAGCTTTTCGGGAAGCCCTGCACATGGACAGGTACCTG
 TTGCTGCACCCAGACTTTCTCCGATACATGAAGAACAGGTTTCTGAGGCTTAAGACCTTGA
 TGGTGCCCACTGGAGGATATACCGCCCCACCCTGGGGCCCTCCTGCTGCTCACTGCCCTT
 AGCTCTGTGACCAGGTGAGTGTCTTATGGCTTCATCACTGAGGGCCATGAGCGCTTTTCTGAT
 CACTACTATGATACATCATGGAAGCGGCTGATCTTTACATAAACCATGACTTCAAGCTGGA
 GAGAGAAGTCTGGAAGCGGCTACACGATGAAGGGATAATCCGGCTGTACCAGCGTCTGGTC
 CCGGAAGTGCCAAAGCCAAGAACTGAACCGGGCCAGGGCTGCCATGGTCTCCTTGCTGCTC
 CAAGGCACAGGATACAGTGGGAATCTTGAGACTCTTTGGCCATTTCCCATGGCTCAGACTAA
 GCTCCAAGCCCTTACGAGTTCCAAGGGAACACTTGAACCATGGACAAAGACTCTCTCAAGAT
 GGCAATGGCTAATTGAGGTTCTGAAGTTCTTCACTACATTGCTGTAGGTCCTGAGGCCAGG
 GATTTTAAATTAATGGGGTGATGGGTGGCCAATACCACAAATTCCTGCTGAAAAACACTCTT
 CCAGTCCAAAAGCTTCTGATACAGAAAAAAGAGCCTGGATTACAGAAACATATAGATCTG
 GTTTGAATCCAGATTCGAGTTTACAGTTGTGAAATCTTGAAGGTATTACTTAACTTCACTAC
 AGATTGTCTAGAAGACCTTTCTAGAGGTTATCTGATTCTAGAAGGCTTATACTTGTCTTG
 TCTTTAAGCTATTTGACAACTCTACGTGTTGTAGAAAACCTGATAATAACAAATGATGTT
 GTCCATGGAAGGCCAAATAATTTCTACAGTGAAAAAAGAAAAA

MRSLCWRCRHLSQGVQWSLLAVLVFFLFALPSFIKEPQTKPSRHQRTEENIKERSLQSLAKP
KSQAPTRARRRTTIYAEPAPENNALNTQTQPKAHTTGDGRKEANQAPPEEQDKVPHTAQRAAW
KSPEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTTQGNGGQTRKLTASRTVSEKHQ
KAATTAKTLIPKSQLHMLAPTGAVSTRTRQKGVTTAVIPPKEKKPQATPPPAPFQSPTTQRN
QRLKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKFLPNLTLFLDSRHF
NQSEWDRLEHFAFPFGFMELNYSLVQKVTRFPVPPVQQQLLASLPAGSLRCITCAVVGNGG
ILNNSHMQGEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGFTAFLTSQSLILGNRGFKNP
LGKDVRYLHFLEGRDYEWELEALLMNQTVMSKNLFWFRHRPQEAFFREALHMDRYLLHPDFL
RYMKNRFLRSKTLGDAHWRIRYRPTTGALLLTALQLCDQVSAYGFITEGHERFSDHYDYTSW
KRLIFYINHDFKLEREVWKRLHDEGIIRLYQRPGPGTAKAKN

Cytoplasmic Domain:

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Luminal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

CGATGCGCGGACCCGGGCACCCCTCTCTCTGGGGCTGCTGCTGGTGTCTGGGGCCTTCGCCG
GAGCAGCGAGTGGAAATTGTTCTCGAGATCTGAGGATGAAGGACAAGTTTCTAAACACCT
TACAGGCCCTCTTTATTTAGTCCAAGTGCAGCAAACACTTCCATAGACTTTATCACAA
CCAGAGACTGCACCATTCTGTCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT
GTCAGTCCAGTGTGCATGGAGGATAAGTGAAGCAGACCGTACAGGAGCAGCACACCAGGAGCC
ATGAGAAAGTGCCTTGAAACCAACAGGGAAACAGAAGTATCTTTATACACATCCCTCATGG
ACAAGAGATTTATTTTGCAGACAGACTCTTCATAAGTCCTTTGAGTTTGTATGTTGTG
ACAGTTTGCAGATATATATTCGATAAATCAGTGTACTTGACAGTGTATCTGTCACTTATTT

FIGURE 244

MRGPGHPLLLGLLLVGPSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNT
RDCTIPAYYKRCARLLTRLAVSPVCMEDK

00000000000000000000000000000000

FIGURE 245

GGGCTGGGCCCCGCCGACGTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGAGG
CCCGACCCCGGCCGCGCCAGCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCCGCGCCG
CTCACCACAATCGCTCTGTTGGTGCTGGGGGCTCCCTGGTGCTGGCCGGCAGGACTGCCT
GTGGTACCTGGACCGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTTCACCTTCT
GCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTATCACCAGAGG
CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT
CCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTCCCTGTTGCTACCTGT
ACCGCCGGCGCCAGCAGCTCCAGAGCCCATTGAAGGCCAGGAGATTCCAATGACAGGCATC
CCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCCAAAGCTGGCCCTGCACCCCCACAGCC
TGGCTTCATGTACCCACCTAGTGGTCCTGCTCCCCAATATCCACTCTACCCAGCTGGGCCCC
CAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC
TGAGGAACCAGCCATGTCTCTGCTGCCCTTCAGTGATGCCAACCTTGGGAGATGCCCTCAT
CCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGTCTCCAGCCACCAGGCCCCAGACCAA
GCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCCAGGGAAGTGGAACAGGAGCTGAACTAGA
ACTATGAGGGGTTGGGGGGAGGGCTTGAATTATGGGCTATTTTTACTGGGGCAAGGGAGG
GAGATGACAGCCTGGGTACAGTGCCTGTTTTCAAATAGTCCCTCTGCTCCCAAGATCCCAG
CCAGGAAGGCTGGGGCCCTACTGTTTGTCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGT
TCCGTCAGCAGCTGGCAGTAGCCCTCCTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTG
CTAGATTAAAGCTGTAAAGACAAAA

FIGURE 246

MPPAGLRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRGSHWPGFNCEFFTFCCGTCYHRYC
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICFLCSCCYLYRRRQQLQSP
FEGQEIPMTGIPVQPVYYPYQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYNPAAPP
YMPPQPSYPGA

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93

GGGGGAGCTAGGCCGGGGGCGAGTGGTGGTGGCGCGCGGCACAAGGGTAGGGCGCGGCCACGAA
CCCCAGGCTAGGTAGTACAGCAAGAAGATGGTGGTGGTTCCTGCCCTCAAAATGGTCCCTTGCAACCATG
TCATTTCCTACTTCTCAGTCTGTTGGCTCTCTTAATGTGTCTCACTCCCTCATGGTGTTCAGAG
CTAGCAGAAGCATCTCCAAAAGCATGTGATGGGACACCATTTCTTGGAAATAAAATACGACTCT
CTGAGTAGCTCATCCCAAGTTCATTATGATCTCTTTGATCATGCAAACTTACACCGCTGACC
TTCTGGGGAAACCCAGAAAGTAGAATACAGCCAGCTAGCCGCCACCCAGACCAATCATCTCGG
TAGTCAACCACTTCGAGATATCTTAGGCCCACTCAGGAAGGGAGCTGGAGAGAGGGCTATCGG
AAGAACCCTTCGAGTCCCTGGGAACCCCTCAGGAGCAAAATGTCATCTCTGGCTCCCGAG
CCCCTCTTGTGGCTCCCGTACACAGTTGTCTTACATGCTGGCAATCTTTGGAAGA
TTTCCACGGATTTTACAAAAGCACTACAGAACCAAGGAAGGGAATGAGATATACGACA
CAACACAATTTGAACCCATCGACGTAGAAATGGCTTTCCCTGGCTTGTGAGCTGCCCTC
AAGACAAGTTTCTCAATCAAAATAGAAGAGAGCCAGGACCTAGCCATCTCCAATATGCC
ATTGTTGAAATCTGTGACTTGTGTCTGAAGGACCTCATAGAAGACATTTGTATGTTCACGTGGA
AGATGAGCAACCTATCTGGTGGCTTCATCATTTTCAGATTTTGAAGTCTGACGAAGAATAACC
AAGATGGGATCAAGGTTTCTGTTTATGTCTGTGCCAGACAAGATAAATCAAGGAGATTATGC
ACTGATGCTCGCGTGACTCTTCTAGAATTTTATGAGATTATTTTCAGATACCGTATCCCC
TACCCAAACAGATATGCTGTGCTATTTCCGAGCTTTTCAGTCTGGTGTCTATGGAAGAACTGGGA
CTGACAACATATAGAAATCTGCTCTGTTGTTTGTATGCAGAAAGTCTTTTCGATCAAGTAA
GCTTGGCATACAGTGAATCTGTGGCCCATGAATGGCCACCAGTGGTTTGGGAAGCTGTGTCA
CTATGGAATGGTGGAAATGATCTTTGGCTAAATGAAGGATTTGCCAAATTTATGGAGTTTGTG
TCTGTTCAGTGTGACCCATCTGACTGAAAGTTGGAGATTATTTCTTGGCAATGTTTGTGA
CGCAATGGAGGTAGATGCTTTAAATTCCTACACCCCTGTGCTACACCTGTGGAAATCCCTG
CTCAGATCGGGAGATGTTTGTATGATGTTTCTTATGATAAGGAGCTTGATTTCTGAATATG
CTAAGGGAGTATCTTAGCGCTGACGCAATTTAAAGAGTGGTATTTGACAGTATCTCCAGGAAGCA
TAGCTATAAAAAATACAAAACAGGAGCTGTGGGATAGTAGTGAAGAATATTTGCCATACAG
ATGGTGTAAAGGAAGTGAATGGCTTTTGTCTAGAAGTCAACATTCATCTTCATCTCACAG
TGGCATCAGGAAGGGGTGGATGTGAAAACCATGTGAACATTTGACATGCAAGTGGCAGGGGTTT
TCCCCTAATAACCATCAAGTGAGGGGAGGAATGTACACATGAAGCAGAGCACTACATGA
AGGGCTCTGACGGCGCCCGGACACTGGGTACCTTGGCATGTTCCATTGACATTCATCAC
AGCAAAATCCAAATATGTCATCGATTTTGGCTAAAACAAAAACAGATGTGCTCATCTCTCC
AGAAGAGGTGGAATGGATCAAAATTAATGTGGGCATGAATGGCTATTACATTTGTCATTACG
AGGATGATGATGGGCACTCTTGACTGGCTTTTAAAGAGAACACACACAGCAAGCTCAGCAGT
AATGATCGGCAAGTCTCATTAACAATGCATTTCACTGCTCAGCATTTGGGAAGCTGTCCAT
TGAAAGGCTCTGGATTTATCCCTGTACTTTGAAACATGAACTGAAATTTATGCCGTTGTTT
AAGGTTTGAATGAGCTGATTTCTATGTATAGTTTAAATGAGAAAGAGATATGAATGAAGTG
GAAATCAATTTAGGCGTCTCTCATCAGCGTCTTAAGGACCTCATTGATAAGCAGACATG
GACACACAGGGGCTCAGTCTACAGACAAATGCTCGGAGTGAACTACTCTCTCGCTGTG
TGACACAACTCATAGCCGCTGCTGACAGAGGCGAAGGCTATTTCAAGAAATGGGAAGGAATC
AATGGAACCTTGAGCCTGCTCTGTCAGCTGAATTTGCGAGTGTGTTGCTGTGGGGCGCCAG
CAGCAAGGCTGGGATTTCTTTATAGTAAATATCAGTTTCTTCTTCACTACTGAGAAA
GCCAAATGAAATTTGCCCTCTGCAAGAACCAAAATTAAGGAAAAGCTTCAATGGCTACTAGAT
GAAAGCTTTAAGGGAGATAAAATAAAACCTCAGGAGTTTCCACAAAATCTTGAACTATTGG
CAGGAACCCATAGGATACCACTGGGCTGGCAATTTCTGAGAAAACCTGACACAAACCTG
TACAAAAGTTTGAATCTGGCTCATCTTCATAGAGCCCATGGTAAATGGGTACACAAATCAA
TTCTCCACAGAACAACCGGCTGGAAGAGTTAAAGGATCTTCAGCTCTTTGAAAGAAAATG
TTCTCAGCTCGGTTGTGTCACACAGCAATTTGAAACCATTAAGAGAAACATCGTTGTAGTGG
ATAAGAATTTCTATAAAATCAGAGTGTGGCTGGAAGTGAAGACTTGAAGTATGTGTA
TTCTTCCTTGGCCGGTTCTGTTTACTCTTAATCACCACATTTTGTGAGTGTATTTTGA
ACTAGAGTATGGCTGTTTGGCTCCAATGGAGATACCTTTTCCCTCAACTCATTTTGA
CTATCCCTGTGAAAGAATAGCTGTAGTTTTCATGAATGGGCTTTTTCATGAATGGGCTA
TCGCTACCACTGTGTTTGTTCATCAGAGTGTGGCTCGCAAGCTAAACCCAGTGTGGGT
TCCCTGCCACAGAAGAAATAGTACCTTATTCTCTCAAAAAAATAAAAAAATAAAAAA

MVFLPLKWSLATMSFLLSLLALLTVSTPSWCQSTEASPKRSDGTFPPWNKIRLPEYVIVPVI
YDLLIHANLTTLTFTWGTTKEVITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPLQVLE
HPPQEQIALLAPEPLLVGLPYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA
ARMAFFCFDEPAFKASFSIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVVA
FIISDFESVSKITKSGVKVSUYAVPDKINQADYALDAAVTLLEFYEDYFSIPYPLPKQDLAA
IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHELAHQWFGNLVMTMEWNNDL
WLNEGFAKMEFVSVSVTHPELVKGDYFFGKCFDAMEVDALNSSHPVSTFVENPAQIREMFD
DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICTPTDGVKGMDG
FCSRSQHSSSSSHWHQEGVDVKTMMNTWTWLQRGFPLITITVGRNVHMKQEHYMKGSDGAPD
TGYLWHVPLTFTITSKSNMVHRFLLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSL
TGLLKGTHTAVSSNDRASLINNAFQLVSIGKLSIEKALDLSLYLKHETEIMPVFQGLNELIP
MYKLEMKRDMNEVETQKAFILRLRLDLIDKQTTWDEGSVSEQMLRSELALLACVHNYQPCV
QRAEGYFRKWKESNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSSTESKQIEFALC
RTQNKEKLQWLLDESFKGDKIKTQEFFQILTLIGRNPVGYPFLAWQFLRKNWNKLQVKFELGS
SSIAHMVMGTTNQFSTRTRLEEVKGFFSSLKENGSQLRCVQQTITETIENIGWMDKNFDKIR
VWLOSEKLERM

amino acids 1-34

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

amino acids 350-360

FIGURE 249

CAGCCACAGACGGGTCA**ATG**AGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCAC
 TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC
 GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCCAGACGGCTTGGGGTGCCAGGA
 CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG
 AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC
 TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
 TTGGGCCCCACAGCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG
 AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGAT
 GGCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
 CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCGTGGGTATGACTGAGA
 ACTGCAATAGGAAAGATTTTCTGACCTGTCTATCGGGGACCACCATTATGACACACGGAAAC
 TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT
 GTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCTTGGTGGGGACAAAAG
 GCTGCAGCACTGTTGGGGCTCAAAATTCAGAGAAGACCACCATCCACTCAGCCCCTCCTGGG
 GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
 CAGCGTTCTGCTGAACTCCCTCCCTCAAGCTGCCCCGTGCCAGGAGACCGGCAGTGTC
 CTACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG
 GCGCCACTCATTGTTATGATGGGTACATTCTCTCAGGAGGTGGGCTGTCCACCAAAAT
 GAGCATTACAGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTGAACCACACCAGACAAATCG
 GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT
 GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG
 GTGGGGAGTGGTTTGCCCTTCCTGCT**TAA**CTCTATTACCCCCACGATTCTTCACCGCTGCTGA
 CCACCCCACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTC
 CCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCA
 AACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTG
 GCTGCATGTATCTGATAATACAGACCCTGTCCTTTCA

FIGURE 251

GCGACGGGCAGGACGCCCCGTTTCGCCTAGCGCGTGCTCAGGAGTTGGTGTCTCGCTGCGCT
CAGG**ATG**AGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCCTGTCACTGCTG
CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTCGTCCCTGG
CCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCCGACGGCCTGGAAGAGTGG
GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGGTCTCAT
GAAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC
TGGTCCTAATGGAGAACCAGGCCTCCCATTGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG
AGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTCGCC
GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA
CGCCAGCTGTCTGCCAGGGCCGCGGGGCGACGCTGAGCATGCCCAAGGACGAGGCTGCCA
ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTGGCCCCGTGTCTTCATCGGCATCAAC
GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCATGCGGACCTTCAACAA
GTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGGACTGCGTGGAGATGGTGGCCT
CGGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTTGACAAG
GAGAACATG**TGA**GCCTCAGGCTGGGGCTGCCCATTTGGGGCCCCACATGTCCCTGCAGGTT
GGCAGGGACAGAGCCAGACCATGGTGCCAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAG
GCTCACTGAGTAGAGGGCTGTTGTCTAAACTGAGAAAATGGCCTATGCTTAAGAGGAAAATG
AAAGTGTTCCCTGGGGTGCTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA
ATGTCATTATGTAATTATTACCCAGAATTGCTCTTCATAAAGCTTGTGCCTTTGTCCAAGC
TATACAATAAAATCTTTAAGTAGTGCAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAAA

FIGURE 253

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG
CACCAGTGTGTGAGGGGAGCAGGCAGCGGTCCTAGCCAGTTCTTTGATCCTGCCAGACCACC
CAGCCCCCGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGTGCTATTACAGCCAT
CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG
TTCCTGGCGGGGGCCGCAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC
AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA
GGAATCAACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA
GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCTCGGCCC
CTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACC
TTTATTAAGACTCTCTACGGATGTGAATCAAGAGAACGTCCCAGCTTTGGGCATCCTCAAGT
ATCCCCCGAGAGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTC
TTTCCCTGTCCCAATCCCAGGTGCGCAGCTCCTGTTACCTTTTCTTCCCTGTTCTTGT
AACATTCTTGTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCCTGGTGTGGAAACTGCA
TAGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCTGTAGTGT
CCTACATTAAAAATATAATGTCTCTCTATTCCTCAACAATAAAGGATTTTTCATATGAA
AA

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MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDL YQLLQRLFKSHSSLEGLLK
ALSQASTDPKESTSPEKRD MHDFVGLMGKRSVQPEGKTGFPLPSVRVPRPLHPNQLGSTGK
SSLGTEEQRPL

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

[illegible]

FIGURE 256

MSCVLGGVPLGLLFLVCGSQGYLLPNVTLLLEELLSKYQHNEHSRVRRAIPREDKEEILML
HNKLRGQVQPQASNMEYMVVSAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGLRVSSGR
GGSRLCSVLFVCFETGSHSATDAGVQVHNHRHALKP

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACT**ATG**GG
GTCTGGGCTGCCCCTTGTCTCCTCTTGACCTCCTTGGCAGCTCACATGGAACAGGCGCG
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGC
TTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCATCTCCCTCAGGGACCAGCGTCAC
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACAT**TGA**CAGCCATTGAAGCCTG
TGTCCTTCTTGGCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCGACCTGTCTTT
CAGCAGGCCCCACCTCCTGAGTGGCAATAAATAAAATTTCGGTATGCTG

FIGURE 261

GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGGAGCCCTTGAGACATCCTT
 GAGAAGAGCCACAGCATAAGAGACTGCCCTGCTGGTGTTTTGCAGG**ATG**ATGGTGGCCCTT
 CGAGGAGCTTCTGCAATTGCTGGTTCTGTTCCCTTGACAGCTTTTCTGCCCCCGCCGAGTGTAC
 CCAGGACCCAGCCATGGTGCAATACATCTACCAGCGCTTTCGAGTCTTTGGAGCAAGGGCTGG
 AAAAAATGTACCCAAGCAACGAGGGCATACATTCAAGAATTCCAAGAGTTCTCAAAAAATATA
 TCTGTCTATGCTGGGAAGATGTCAGACCTACACAAGTGAGTACAAGAGTGCAGTGGGTAACCTT
 GGCATGAGAGTTGAACGTCGCCAACGGGAGATTGACTACATACAATACCTTCCGAGAGGCTG
 ACGAGTGCATCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAA
 GAGAAAAAGATCCGGACTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTC
 TTTGAAAATAGTGAAGAAGATGATGGACACACATGGCTCTTGGATGAAAGATGCTGCTCTATA
 ACTCTCCAAAGGTGTACTTATTAATTGGATCCAGAAACAACACTGTTTGGGAATTTGCAAAC
 ATACGGGCATTTCATGGAGGATAACACCAAGCCAGCTCCCCGGAAGCAAATCCTAACACTTTC
 CTGGCAGGGAACAGGCCAAGTGATCTACAAAGGTTTCTATTTTTTCATAACCAAGCAACTT
 CTAATGAGATAATCAAAATAAACCTGCAGAAGAGGACTGTGGAAGATCGAATGCTGCTCCCA
 GGAGGGGTAGGCCGAGCATTGGTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGT
 GGATGAGCATGGGCTCTGGGCCATCCACTCTGGGCCAGGCCATAGCCATTGGTTCTCA
 CAAAGATTGAGCCGGGCACACTGGGAGTGGAGCATTCATGGGATACCCCATGCAGAAGCCAG
 GATGCTGAAGCCTCATTCTCTTGTGTGGGTTCTCTATGTGGTCTACAGTACTGGGGCCCA
 GGGCCCTCATCGCATCACCTGCATCTATGATCCACTGGGCACTATCAGTGAGGAGGACTTGC
 CCAACTTGTTCCTTCCCCAAGAGACCAAGAAGTCACCTCCATGATCCATTACAACCCAGAGAT
 AAGCAGCTCTATGCCTGGAATGAAGGAAACCAGATCATTTACAAACTCCAGACAAAGAGAAA
 GCTGCCTCTGAAG**TAA**TGCATTACAGCTGTGAGAAAGAGCACTGTGGCTTGGCAGCTGTTC
 TACAGGACAGTGAGGCTATAGCCCCCTTCACAATATAGTATCCCTCTAATCACACACAGGAAG
 AGTGTGTAGAAGTGGAATACGTATGCCCTCTTCCCAAAATGTCACTGCCCTTAGGTATCTTC
 CAAGAGCTTAGATGAGAGCATATCATCAGGAAAAGTTTCAACAATGTCCATTACTCCCCCAAA
 CCTCCTGGCTCTCAAGGATGACCACATTCTGATACAGCCTACTTCAAGCCTTTTGTCTTACT
 GCTCCCCAGCATTTACTGTAACTCTGCCATCTTCCCTCCCAATTAGAGTTGTATGCCAGC
 CCTAATATTACCACTGGCTTTTCTCTCCCTGGCCTTGTGTAAGCTCTTCCCTCTTTTT
 CAAATGTCTATTGATATTCTCCCATTTTCACTGCCCAACTAAAATACATTAAATATTCTTT
 CTTTTCTTTTTCTTTTTTTTGGAGACAAGGTCTCACTATGTTGCCAGGCTGGTCTCAAACCTC
 AGAGCTCAAGAGATCCTCCTGCCTCAGCCTCCTAAGTACCTGGGATTACAGGCATGTGCCAC
 CACACCTGGCTTAAATACATTTTCTATTGAGGTTTAACTCTATTTCCCCTAGCCCTGTC
 CTTCCACTAAGCTTGGTAGATGTAATAATAAAGTGAAATATTAACATTGAAATATCGCTTT
 CCAGGTGTGGAGTGTTCACATCATTTGAATCTCGTTTTACCTTTGTGAAACATGCACAAG
 TCTTTACAGCTGTCACTTAGAGTTTAGTGAGTGAACACAATACAAAGTGAAAGATACAGC
 TAGAAAAATACATAAATCCCATAGTTTTTCCATTGCCCAAGGAAGCATCAAATACGTATGTT
 TGTTCACCTACTCTTATAGTCAATGCGTTCATCGTTTCAGCCTAAAAATAATAGTCTGTCC
 TTTAGCCAGTTTTTCAATGCTGTGCACAAGACCTTTCAATAGGCCTTTCAAATGATAATCTCC
 AGAAACCAAGTCTAAGGGTGAGGACCCCAACTCTAGCCTCCTCTGTCTGTCTGCTCTGT
 TTCTCTCTTCTGCTTTAAATTCAATAAAAGTGACACTGAGCAAAAAAAAAAAAAA

GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGGAGCCCTTGAGACATCCTT
 GAGAAGAGCCACAGCATAAGAGACTGCCCTGCTGGTGTTTTGCAGG**ATG**ATGGTGGCCCTT
 CGAGGAGCTTCTGCAATTGCTGGTTCTGTTCCCTTGACAGCTTTTCTGCCCCCGCCGAGTGTAC
 CCAGGACCCAGCCATGGTGCAATACATCTACCAGCGCTTTCGAGTCTTTGGAGCAAGGGCTGG
 AAAAAATGTACCCAAGCAACGAGGGCATACATTCAAGAATTCCAAGAGTTCTCAAAAAATATA
 TCTGTCTATGCTGGGAAGATGTCAGACCTACACAAGTGAGTACAAGAGTGCAGTGGGTAACCTT
 GGCATGAGAGTTGAACGTCGCCAACGGGAGATTGACTACATACAATACCTTCCGAGAGGCTG
 ACGAGTGCATCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAA
 GAGAAAAAGATCCGGACTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTC
 TTTGAAAATAGTGAAGAAGATGATGGACACACATGGCTCTTGGATGAAAGATGCTGCTCTATA
 ACTCTCCAAAGGTGTACTTATTAATTGGATCCAGAAACAACACTGTTTGGGAATTTGCAAAC
 ATACGGGCATTTCATGGAGGATAACACCAAGCCAGCTCCCCGGAAGCAAATCCTAACACTTTC
 CTGGCAGGGAACAGGCCAAGTGATCTACAAAGGTTTCTATTTTTTCATAACCAAGCAACTT
 CTAATGAGATAATCAAAATAAACCTGCAGAAGAGGACTGTGGAAGATCGAATGCTGCTCCCA
 GGAGGGGTAGGCCGAGCATTGGTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGT
 GGATGAGCATGGGCTCTGGGCCATCCACTCTGGGCCAGGCCATAGCCATTGGTTCTCA
 CAAAGATTGAGCCGGGCACACTGGGAGTGGAGCATTCATGGGATACCCCATGCAGAAGCCAG
 GATGCTGAAGCCTCATTCTCTTGTGTGGGTTCTCTATGTGGTCTACAGTACTGGGGCCCA
 GGGCCCTCATCGCATCACCTGCATCTATGATCCACTGGGCACTATCAGTGAGGAGGACTTGC
 CCAACTTGTTCCTTCCCCAAGAGACCAAGAAGTCACCTCCATGATCCATTACAACCCAGAGAT
 AAGCAGCTCTATGCCTGGAATGAAGGAAACCAGATCATTTACAAACTCCAGACAAAGAGAAA
 GCTGCCTCTGAAG**TAA**TGCATTACAGCTGTGAGAAAGAGCACTGTGGCTTGGCAGCTGTTC
 TACAGGACAGTGAGGCTATAGCCCCCTTCACAATATAGTATCCCTCTAATCACACACAGGAAG
 AGTGTGTAGAAGTGGAATACGTATGCCCTCTTCCCAAAATGTCACTGCCCTTAGGTATCTTC
 CAAGAGCTTAGATGAGAGCATATCATCAGGAAAAGTTTCAACAATGTCCATTACTCCCCCAAA
 CCTCCTGGCTCTCAAGGATGACCACATTCTGATACAGCCTACTTCAAGCCTTTTGTCTTACT
 GCTCCCCAGCATTTACTGTAACTCTGCCATCTTCCCTCCCAATTAGAGTTGTATGCCAGC
 CCTAATATTACCACTGGCTTTTCTCTCCCTGGCCTTGTGTAAGCTCTTCCCTCTTTTT
 CAAATGTCTATTGATATTCTCCCATTTTCACTGCCCAACTAAAATACATTAAATATTCTTT
 CTTTTCTTTTTCTTTTTTTTGGAGACAAGGTCTCACTATGTTGCCAGGCTGGTCTCAAACCTC
 AGAGCTCAAGAGATCCTCCTGCCTCAGCCTCCTAAGTACCTGGGATTACAGGCATGTGCCAC
 CACACCTGGCTTAAATACATTTTCTATTGAGGTTTAACTCTATTTCCCCTAGCCCTGTC
 CTTCCACTAAGCTTGGTAGATGTAATAATAAAGTGAAATATTAACATTGAAATATCGCTTT
 CCAGGTGTGGAGTGTTCACATCATTTGAATCTCGTTTTACCTTTGTGAAACATGCACAAG
 TCTTTACAGCTGTCACTTAGAGTTTAGTGAGTGAACACAATACAAAGTGAAAGATACAGC
 TAGAAAAATACATAAATCCCATAGTTTTTCCATTGCCCAAGGAAGCATCAAATACGTATGTT
 TGTTCACCTACTCTTATAGTCAATGCGTTCATCGTTTCAGCCTAAAAATAATAGTCTGTCC
 TTTAGCCAGTTTTTCAATGCTGTGCACAAGACCTTTCAATAGGCCTTTCAAATGATAATCTCC
 AGAAACCAAGTCTAAGGGTGAGGACCCCAACTCTAGCCTCCTCTGTCTGTCTGCTCTGT
 TTCTCTCTTCTGCTTTAAATTCAATAAAAGTGACACTGAGCAAAAAAAAAAAAAA

FIGURE 262

MMVALRGASALLVLFLLAFLPPPQCTQDPAMVHYIYQRFVLEQGLEKCTQATRAYIQEFQE
FSKNISVMLGRCQTYTSEYKSAVGNLALRVERAQREIDYIQYLREADECIVSEDKTLAEMLL
QEAEKKKIRITLLNASCDNMLMGIKSLKIVKKMMDTHGSWMKDAVYNSPKVYLLIGSRNNTV
WEFANIRAFMEDNTKPAPRKQILTLSWQGTGQVIYKGFLFFHNQATSNEIIKYNLQKRTVED
RMLLPGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEPGLGVEHSWDT
PCRSQDAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFPPKRPRSHSMIH
YNPRDKQLYAWNENQIIYKLQTKRKLPLK

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GGGCGCCCGCGTACTCACTAGCTGAGGTGGCGTGGTTCCACCAACATGGAGCTCTCGCAGA
TGTCGGAGATCTGATGGGGTGTCGCTGTGTGCTTGGGCTGCTGGCCCTGATGGCCAGCGCGCG
GTAGCGCGGGGGTGCTGCGCGCGGGGAGGAGGAGCGCGCGCGCGCTGCCAAAAGC
AAATGGATTTCCACCTGACAAATCTTCGGATCCAAGAAGCAGAAACAATATCAGCGGATTC
GCAGGAGAAAGCACTCAACACACAACTCACCACCGCCTCCTGGCTGCAGCTCTGAAGAGC
CAGACGGGGAACATATCTTGATGCTGACTTTAGCAGCAATGGCAAAATACTGGCTACCTGTGC
AGATGATCGCACCATCCGCATCTGGAGCACCAGGACTTCCTGCAGCGAGAGCACC CGCAGC
TTAGACCAACCTGAGGACTGGACACGCCACCTTGTGCGCTTGACGCTTACTGCTGAGAGACC
TGATCTGCTTGGCTGGCCAACGGGACACCTTCGTGTCTTCAAGATGACCAAGCGGGAGGA
TGGGGGCTACACCTTCACAGCCACCCAGAGGACTTCCTTAAAAAGCAAGGCGCCTGTCA
TCGACATTTGGCATTTGCTACACAGGGAAGTTTATCATGACTGCTCCTGATGACACCTGTC
CTCATCTGGAAGCCTGAAGGTCAAGTGCTGTCCACCTAACCAACCAACAGATGAACAACAC
ACACGCTGCTGTATCTCCCTGTGGCAGATTGTGAGCCTCGTGTGGCTTACACCCAGATGTGA
AGGTTTGGGAAGTCTGCTTTGAAAAAGAGGGGAGTTCAGGAGTGGTGCAGCCTTCGAA
CTAAAGGGCCACTCCGCGCTGTGCACTCTTGTCTTTTCCACAGCTACCGGAGATTGCG
TTCTGTGCTCAAGGATGGTACATGGAAACTGTGGGACACAGATGTGGAATACAGAAGAAGC
AGGACCCCTACTTGCTGAAGACAGCCGCTTTGAAGAGCGCGCGGCTGCCGCGCTGCCGC
CTGGCCCTTCTCCCCACAGCCAGGCTTGGCTTGGCCACTGGGAGTAGTATTATCTCTCA
AAATACCCGCGGGCGAGAGGAGGAGTGTCTTTGAGCGGGTCCATGGCGAGTGTATGCCA
ACTTGTCTTTGACATCACTGGCGCTTTCTGGCTCCTGTGGGACCGGGCGGTGCGGCTG
TTTCAACAACACTCTGGCCACAGGCTTGGTGAGGAGATGCGGCGCCACTGAAGCGGGC
CTCCAACGAGAGACGCCGCCAGAGGCTGAGGAGCAGCTGACCCAGGCCAACAGACCTGA
AGAGCCTGGGTGCCCTGAAGAAGTGACTACTTGGGAGGGCCCGGCCGACAGGATTGAGGAGGAG
GGATCTGGCCCTCTCATGGCACTGCTGCCATCTTCTCCAGGTGGAAGCTTTTCAAGAG
AGTCTCTGTGTTTTCTTACTTGTGGCCCTGCTCTTCCATTGAACACTCTTGTCTACTT
AGGTCTCTCTCTTCTTGTGCTGGCTGTGACTCCTCCTGACTAGTGCCCAAGGTGCTTTTCTC
CTCCCAGGCCCACTGGGTGGAATCTGTCCCCACTGGCACTGAGGAGAAATGGTAGAGGAG
AGGAGACAGAGAGAGAAATGTGATTTTGGCCTTGTGGACGACATCCTACACCCAAAGAG
TTTGTAATGTTCAGAACAACTTAGAGAACACCTGAGTACTAAGCAGCAGTTTTTGCAAGGA
TGGGAGACTGGGATAGCTTCCCATCACAAGAACTGTTCCTCAAAAAGACACTAAGGGATT
TCCTTCTGGGCTCAGTTCTATTGTGAAGTGGAATAATCCTCTCTGTAACCTTATGTGA
AAGTACTATATGAGGCTAAGAGAAATCAAGTCCCCAGGCTTGAAGAGAAAGTAGAAAAGAT
AGTACTATTGTCCAATGCTCATGAAAGTGTTAAAGTGGGAACCAAGTGTCTTTGAAACCAA
TTAGAACACATCTCTGGGAAGGCAAAGTTTCTGGGACTTGATCATACATTTATATGGT
TGGGACTTCTCTCTCGGGAGATGATATCTGTTTAAAGAGACCTCTTTTCAGTTTCATCAAG
TTTCATCAGATATTGAGTGCCCACTCTGTGCCCAATAAATAATGAGCTGGGGATTAAAAAA
AA

FIGURE 264

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPPDKSSGSKKQK
QYQIRIRKEKPQQHNFTHRLLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ
REHRSMRANVELDHATLVRFSPDCRAFIVWLANGDTLRVFKMTKREDGGYTFTATPEDFPKK
HKAPVIDIGIANTGKFIMTASSDTTVLIWSLKGQVLSTINTNQMNNTHAAVSPCGRFVASCG
FTPDKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV
EYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVH
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHLKRASNESTRQLQQQLTQ
AQETLKSLGALKK

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

FIGURE 265

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG
 CAGTGTTTTGCCTTCACCCCAAGTGACCATGAGAGGTGCCACGCGAGTCTCAATCATGTCTC
 TCCTAGTAACGTGTGTCTGACTGTGCTGTGATCACAGGGCCTGTGAGCGGGATGTCCAGTGT
 GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGCACCCCGCT
 GGGGCGGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGTCCCCTTCTTCAGGAAACGCA
 AGCACACACCTGTCTTGCTTGCCCAACCTGCTGTGCTCCAGGTCCCAGGACGGCAGGTAC
 CGCTGCTCCATGGACTTGAAGAACATCAATTTTTAGGCGCTTGCCCTGGTCTCAGGATACCCA
 CCATCCTTTTCTGAGCACAGCCTGGATTTTATTTCTGCCATGAAACCCAGTCCCATGAC
 TCTCCAGTCCCTACACTGACTACCTGATCTCTCTTGTCTAGTACGCACATATGCACACAG
 GCAGACATACCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTACAGCTTGAGG
 CTGTGGTGTGAAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTA
 AATGGCAGAAAGGACATTCCCCCTCCCCAGGTGACCTGCTCTCTTCTGGGCCCTG
 CCCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCCCTGGGCACAGGCTCTTGGGT
 GCATTGCTCAGAGTCCCAGGTCCTGGCCTGACCCTCAGGCCCTTCACGTGAGGTCTGTGAGG
 ACCAATTTGTGGGTAGTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGAC
 TCAAGATTGGCTCTTCCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCA
 GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTTGTGGCCTGTGA
 CCTGTGACCTTCTGCCAGAATTGTGCATGCCTCTGAGGCCCCCTCTTACCACACTTTACCAGT
 TAACCACTGAAGCCCCAATTCCACAGCTTTTCCATTAAATGCAAATGGTGGTGGTTCAA
 TCTAATCTGATATTGACATATTAGAAGGCAATTAGGGTGTTCCTTAAACAACCTCCTTTCCA
 AGGATCAGCCCTGAGAGCAGGTGGTGACTTTGAGGAGGGCAGTCCTCTGTCCAGATTGGGG
 TGGGAGCAAGGGACAGGGAGCAGGGCTGAAAGGGGCACTGATTCAGACCAGGGAGG
 CAACTACACACCAACATGCTGGCTTTAGAATAAAAGCACCAACTGAAAAA

FIGURE 266

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEETCH
GSHKVPFFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

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FIGURE 267

AGGCGCCGGGCGCTCGGGGCGGTAAAAGGCCGCAGAAAGGAGGCACTTGAGAAATGCTCTTTT
 CTCCAGGACCCAAGTTTCTTACCATTGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGC
 TGCTGCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTTCTGTCCAAGCCCCAGAAAGCGG
 CCCTGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAAA
 GCAAAGGAGCTATGGGAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTT
 CCTCTGTCGAGAGGAAGCTCGGATCTGTCTCCTGAAAAGCATGTTGGACCAGCTGGGCG
 TCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTAT
 TTCAAAGGAGAAATCTTCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGCGGAAGAT
 GATGTTTATGGGATTATCCGCTCTGGGAGTGTGGTACAACCTTCTCCGAGCCTGGAACGGAG
 GCTTCTCTGGAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTCTGTGGTGGGATCA
 GGAAAGCAGGGCATTCTTCTTGAGCACCAGAAAAAGAATTTGGAGACAAAGTAAACCTACT
 TTCTGTTCTGGAAGCTGCTAAGATGATCAAACCACAGACTTTGGCCTCAGAGAAAAATGAT
 TGTGTGAAACTGCCAGCTCAGGGATAACCAGGGACATTACCTGTGTTCATGGGATGTATT
 GTTTCCTACTCGTGTCCCTAAGGAGTGAGAAACCCATTTATACTCTACTCTCAGTATGGATTA
 TTAATGTATTTTAATATTCTGTTTAGGCCCACTAAGGCAAAATAGCCCCAAAACAAGACTGA
 CAAAAATCTGAAAACTAATGAGGATTATTAAGCTAAAACCTGGGAAATAGGAGGCTTAAAA
 TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCAGCACTTTGGGAGGCCAAGG
 TGAGCAAGTCACTTGAGGTCGGGAGTTCGAGACCAGCCTGAGCAACATGGCGAAACCCGTC
 TCTACTAAAAATACAAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCG
 GGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCA
 CACCACTGTATTCCAGCCTGGGTGACTGAGACTCTAACTAA

FIGURE 268

MSFLQDPSFFTMGMWSIGAGALGAAALALLLANTDVFLSKPQKALEYLEDIDLKTLEKEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSM LDQLGVPLYAVVKEHIRTEVKDF
QPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGVWYNFFRAWNGGFSGNLEGE GFILGGVFV
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

MSFLQDPSFFTMGMWSIGAGALGAAALALLLANTDVFLSKPQKALEYLEDIDLKTLEKEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSM LDQLGVPLYAVVKEHIRTEVKDF
QPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGVWYNFFRAWNGGFSGNLEGE GFILGGVFV
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

FIGURE 269

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCC
GGCCAGGTGCCCCGTCGCAGGTGCCCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGA
AGCCCCCTTCCTCGGCGCTGCCAACCCGCCACCCAGCCCATGGCGAACCCCGGGCTGGGGCTG
CTTCTGGCGCTGGGCCCTGCCGTTCCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACA
GACCACTTCTGCAAAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATG
GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTG
CTCCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG
CACCTACCGGCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGG
ACTCCAAGGAGACGGTGCAGGGCTGCCTGCCCATCTAGGTCCCCCTCTCCTGCATCTGTCTCC
CTTCATTGCTGTGTGACCTTGGGGAAGGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAG
TGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCTGAGGTCAAGAGAGGATGGG
GCTATTCACTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAA

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FIGURE 270

MANPGLGLLLLALGLPFLARWGRAWGQIQTTSANENSTVLPSTSSSSDGNLRPEAITAIIV
VFSLAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

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FIGURE 271

AATATATCATCTATTTATCATTAAATCAATAATGTATTCTTTTATTCCAATAACATTTGGGTT
TTGGGATTTTAATTTTCAAACACAGCAGAAATGACATTTTTCTGTCACTATTATTATTGTTG
GTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCT
ATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC
CTACCAAAGCTGTCAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA
GGGTTAATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATG
ATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATA
TATACAATAAGGTGAAATTATAAGTACCCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT
TTATTAATTTTAAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGA
TCATATAATTTGATACAAATAAAAGAAAAGTGTTCTCTCCCCTTACAGAATTGACATTTTAA
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA
AGAAGGGAAAATGTTGCCAAGGAAAAA

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK
GIVKGRNLDNRGLILGAEAWGRGVKKNT

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK
GIVKGRNLDNRGLILGAEAWGRGVKKNT

FIGURE 273

GCCAGGAATAACTAGAGAGGAACA**ATG**GGGTATTTCAGAGGTTTTGTTTTCTCTTAGTTCT
 GTGCTTGCTGCACCAGTCAAATACTTCCTTCATTAAGCTGAATAATAATGGCTTTGAAGATA
 TTGTTCATTGTTATAGATCCTAGTGTGCCAGAAGATGAAAAATAATTGAACAAATAGAGGAT
 ATGGTGACTACAGCTTCTACGTACCTGTTTGAAGCCACGAAAAAAGATTTTTTTTCAAAAA
 TGTATCTATATTAATTCCTGAGAATTGGAAGGAAAAATCCTCAGTACAAAAGGCCAAAAATG
 AAAACCATAAACATGCTGATGTTATAGTTGCAACCCTACACTCCCAGGTAGAGATGAACCA
 TACACCAAGCAGTTACAGAAATGTGGAGAGAAAGGCCAATACATTCACCTTCACCCCTGACCT
 TCTACTTTGGAAAAAACAAAATGAATATGGACCACCAGGCAAACTGTTTGTCCATGAGTGGG
 CTCACCTCCGGTGGGGAGTGTGTTGATGAGTACAATGAAGATCAGCCTTCTACCGTGCCTAAG
 TCAAAAAAATCGAAGCAACAAGGTGTTCCGCAGGTATCTCTGGTAGAAAATAGAGTTTATAA
 GTGTCAAGGAGGCAGCTGTCTTAGTAGAGCATGCAGAATTGATCTACAACAAAACCTGTATG
 GAAAAGATTGTCAATTCTTTCTGATAAAGTACAAACAGAAAAAGCATCCATAATGTTTATG
 CAAAGTATTGATTCGTTGTTGTAATTTTGTAAACGAAAAACCATATCAAGAAGCTCCAAG
 CCTACAAAACATAAAGTGCAATTTTGAAGTACATGGGAGGTGATTAGCAATTCTGAGGATT
 TTA AAAACACCATACCCATGGTGACACCACCTCCTCCACCTGTCTTCTCATTGCTGAAGAT
 AGTCAAAAGATTGTGTGCTTAGTTCTTGATAAGTCTGGAAGCATGGGGGGTAAAGACCCTCT
 AAATCGAATTGAATCAAGCAGCAAAAACATTTCTGTGTCAGACAGCTGTTGAAAATGGATCCTGGG
 TGGGGATGGTTTCATCTTGATAGTACTGCCACTATTGTAATAAGCTAATCCAATAAAAAAGC
 AGTGATGAAGAAACACACTACCTGAGGATTACCTACATCTCTCTGGGAGGAACCTCCAT
 CTGCTCTGGAATTAATATGCATTTACAGGTGATGGAGAGCTACATTTCCCACTCGATGGAT
 CCGAAGTACTGCTGCTGACTGATGGGGAGGATAACACTGCAAGTCTTGTTGATTGATGAAGTG
 AAACAAAGTGGGGCTATTGTTTCATTTTATTGCTTTGGGAAGAGCTGCTGATGAAGCAGTAA
 AGAGATGAGCAAGATAACAGGAGGAAGTCAITTTTATGTTTCTCAGATGAAGCTCAGAACAATG
 GCCTCATTTGATGCTTTTGGGGCTCTTACATCAGGAAATACTGATCTCTCCAGAAGTCCCTT
 CAGCTCGAAAGTAAGGGATTAAACACTGAATAGTAATGCCTGGATGAACGACACTGTCTATAAT
 TGATAGTACAGTGGGAAAGGACACGTTCTTTCTCATCACATGGAAACAGTCTGCCTCCAGTA
 TTTCTCTCTGGGATCCAGTGGAACAATAATGGAATAATTTACAGTGGATGCAACTTCCAAA
 ATGGCCATATCTCAGTATTTCCAGGAACCTGCAAAGGTGGGCACCTGGGCATACAATCTTCAAGC
 CAAAGCGAACCCAGAAACATTAACATTTACAGTAACCTCTCGAGCAGCAAAATCTTCTGTGC
 CTCCAATCACAGTGAATGCTAAAATGAATAAGGACGTAAACAGTTTCCCGAGCCCAATGATT
 GTTTACGCAAAAATCTACAAGGATATGTACCTGTTCTTGGAGCAATGTGACTGCTTTTCAT
 TGAATCACAGAATGGACATACAGAAGTTTGGAACTTTTGGATAATGGTGCAGGCGTGATT
 CTTTCAAGAATGATGGAGTCTACTCCAGGTATTTTACAGCATATACAGAAAATGGCAGATAT
 AGCTTAAAAGTTCGGGCTCATGGAGGAGCAACACTGCCAGGCTAAAATTTACGGCCTCCAT
 GAATAGAGCCGCGTACATACACAGGCTGGGTAGTGAACGGGGAAATTTGAAGCAAAACCCGCA
 GACCTGAAATTTGATGAGGATACCTCAGACCACCTTGGAGGATTTTCAAGCCGAAACGACATCCGGA
 GGTGCATTTGTGTTATCACAAGTCCCAAGCCTTCCCTTGCCTACGCAATACCCCAAGTCA
 AATCACAGACCTTGATGCCACAGTTTCATGAGGATAAGATTATTTCTACATGGACAGCACCAG
 GAGATAATTTGATGTTGGAAGAAGTTCAACGTTATATCATAGAATAAGTGCAAGTATTTCTT
 GATCTAAGAGACAGTTTTGATGATGCTCTTCAAGTAAATACTACTGATCTGTCAACCAAGGA
 GGCCAACCTCCAAGGAAAGCTTTGCATTTAAACCGAATAATCTCAGAAGAAAATGCAACCC
 ACATATTTATTGCCATTTAAAGTATAGATAAAAGCAATTTGACATCAAAAGTATCCAACAT
 GCACAAGTAACTTTGTTTATCCCTCAAGCAAACTCTGATGACATTTGATCTACACCTACCTC
 TACTCTTACTCTACTCTGATTAAGGATCATAAATCTGAGGATTAATTTTCTACGCTGGTAT
 TGTCTGTGATGGGTCTTGTGTAATTTGTTAACTTTATTTTAAAGTACCACCATTTGAACCTTA
 ACGAAGAAAAAATCTTTCAAGTAGACCTAGAAGAGAGTTTAAAAAACAAAAACAAATGTAAGT
 AAAGGATATTTCTGAATCTTAAATTCATCCATGTGTGATCATAAACTCATAAAAATAAT
 TTAAGATGTGGGAAAGGATACCTTTGATTAATAAAAAACACTCAGGATATGTAAGAACTGT
 CAAGATTAAAAATTTAATGATTTTCATTTATTTGTTATTTTATTTGTAAGAAATAGTGATGAAC
 AAAGATCCTTTTCTACTGATACCTGGTGTATATTTATTTGATGCAACAGTTTTCTGAAAT
 GATATTTCAAAATTCATCAAGAAATTAATCATCTATCTGAGTAGTCAAAATACAAGTAAA
 GGAGAGCAAAATAACAACATTTGAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 274

MGLFRGFVFLVLCLLHQSNSTSFIKLNNNGFEDIVIVIDPSVPEDEKIIIEQIEDMVTTASTY
 LFEATEKRFFFKNVSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTEC
 GEKGEYIHFTPDLLLGGKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATR
 CSAGISGRNRVYKCGGSCLSRACRIDSTTKLYGKDCQFFPDKVQTEKASIMFMQSIDSVVE
 FCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDFKNITPMVTPPPPVFSLKISQRIVCLV
 LDKSGSMGGKDRNLNRNMQAAKHFLQTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLM
 AGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLTGDGDNNTASSCIDEVKQSGAIVH
 FIALGRAADEAVIEMSKITGGSHFYVDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLT
 LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSGTIMENFTVDATSKMAYLSIPG
 TAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKMNDVNSFPSPMIVYAEILQG
 YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNDGVYSRYFTAYTENGRYSLKVRAGH
 GANTARLKLRLPLNRAAYIPGWVNGEIEANPPRPEIDEDTQTTELEDFSRASGGAFVVSQV
 PSLPLPDQYPPSQITDLDATVHEDKIIILTWTAPGDNFDVGKVQRYIIRISASILDRLRDSFDD
 ALQVNTDLSPKANSKESFAFKPENISEENATHIFIAIKSIDKSNLTSKVSANIAQVTLFIP
 QANPDDIDPTPTPTPTPTPKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

FIGURE 275

CTCCTTAGGTGGAACCCCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATACGTCCCCG
 GGCAGGGGTGACAAACAGGTGCATCTTTTGTATCTCGTGTGTGGCTGCCCTTCTATTTCAAGGAAAG
 ACGCCAAGTAATTTTGAACCCAGAGGAGCAATGATGTAGCCACCTCTTAACCTTCCCTTCTTGAACC
 CCCAGTTATGCCAGGATTTACTAGAGAGTGTCAACTCAACAGCAGGCGGCTCCTTCGGCTTAACTT
 GTGGTTGAGAGAGAACCTTTGTGGGGCTGCGTTCTCTTAGCAGTGCTCAGAAAGTGAATTCGCTGATG
 GGGTGGACCAGAAAGAAAGGAGTCCCTCTTGCTGTTGGCTGCACATCAGGAAGGCTGTGATGGG
 AATGAAGGTGAAAACCTTGGAGATTTCACTTCAGTCATTGCTTCTGCTGCAAGATCATCCTTTAAAA
 GTAGAGAAGCTGCTCTGTGTGGTGGTAACTCCAAGAGGCAAGAACTCGTTCTAGAAGGAAATGGATG
 CAAGCAGCTCCGGGGGGCCCCAACGCATGCTTCTGTGGTCTAGCCAGGGAAGCCCTTCCTGGGG
 GCCCCTGGTTTGAAGGATGCCACCGGTTCTGGACGCATGGCTGATTCTCTGAATGATGATGGTTCGCC
 GGGGCTGCTTGCCTGGATTTCCCGGGTGGTGGTTTGTCTGCTGCTCCTCTGCTGTCTATCTCTGT
 CCTGTACATGTTGGCCTGCACCCCAAAGGTGACGAGGAGCAGCTGGCAGCTGCCAGGGCCAAACAGC
 CCCACGGGGAAGGAGGCTACACGGCCGTCTTCAGGAGTGGGAGGAGCAGCCGCAACTACGTGA
 CGACCTGGAAGCGGCAGATCGCAGCTCAAGGAGGAGTGCAGGAGGAGTGAAGCAGCTCAGGAA
 TGGGCAGTACAAGCCAGCGATGCTGCTGGCCTGGGTCTGGACAGGAGGCCCCAGAGAAAACCCAG
 GCGGACCTCCTGGCCTTCTCTGCACCTCGCAGGTGGACAGGCAAGGTGAATGCTGGCGTCAAGCTGG
 CCACAGAGTATGAGCAGGCTGCTTTCGATAGCTTTACTCTACAGAGGTTACACAGCTGGAGACTGG
 CCTTACCCGCCACCCGAGGAGAGCCCTGTGAGGAAGGACAAAGCGGATCAGTTGGTGGAAAGCCATT
 GAATCAGCCTTGAGAGCCCTGAACAACTCTGCAGAGAACAGGCCCAATCAGCTCCTTACACGGCT
 CTGATTTCTATAGAAGGATCTACCGAACAGAAAGGGACAAAGGCAATGTATGAGCTCACCTTCAA
 AGGGACACAAACCAATTCACACCGGCTCATCTTATTTGCAGCATTCAGGCCCATGATGAAGGTG
 AAAAATGAAAAGCTCAACATGGCCCAACACGCTTATCAATGTTATCTGCTGCTTACGAAAAGGGTGG
 ACAAGTTCCGGCAGTTCACTGAGAAATTCAGGGAGATGTGCATTTGAGCAGGATGGGAGAGTCCATT
 CACTGTTGTTTACTTTGGGAAAGAAAGAAATAAATCAAGTCAAAGGAATCTTGAAGAACCTTCAA
 GCTGCCAATCTCAGGAACCTTACCTTCATCCAGCTGAATGGAGAATTTTCTCGGGGAAAGGAGCTG
 ATGTTGGAGCCCCGCTTCTGGAAAGGAAGCAACGCTCCTTCTCTTTTCTGTGATGTGGACATCACT
 CACATCTGAATTCCTCAATACGTGTAGGCTGAATACACAGCCAGGGAAGAGGTATTTTATCCAGTT
 CTTTTCAAGTCAGTACAATCCTGGCATAAATATACGGCCACCATGTGAGCTCCTCTTGAACAGC
 AGCTGGTCATAAAGAAAGGAACTGGATTTTGGAGAGACTTTGGATTGGGATGACGTGTCAATGCTG
 GTCAGACTTCATCAATATAGGTGGGTTTGATCTGGACATCAAAGGCTGGGGCGGAGAGGATGTGCAC
 CTTTATCGCAAGTATCTCCACAGCAACCTCATAGTGGTACGGACGCTGTGCGAGGACTCTTCCACC
 TCTGGCATGAGAAGCGCTGCATGGACGAGCTGACCCCGAGCAGCAAGATGTGCATGCAAGTCCAA
 GGCCATGAACAGAGGCATCCACGCGCAGCTGGGCATGCTGGTGTTCAGGCACGAGATAGAGGCTCAC
 CTTTCGAAACAGAAACAGAAAGCAAGTACGAAAAAACAATGAACCTCCAGAGAAGGATTGGGGAGA
 CACTTTTTCTTTCTTTTGCATTTACTGAAAGTGGCTGCAACAGAGAAAGACTTCCATAAAGGAGC
 ACAAAAGAAATTTGAGCTGATGGGTGAGAGATGAGAAAGCCTCCGATTTCTCTGTGTGGGCTTTTAC
 AACAGAAATCAAATCTCCGCTTTGCTGCAAAAGTAACCCAGTTGCACCTGTGAAGTGTCTGACA
 AAGGCAGAATGCTTGTGAGATTAAAGCCTAATGGTGTGGAGGTTTGTGGTGTTTTCAATAACAT
 GAGACCTGTTGTTTGTGTGCTCATGAAATATTCATGATTAAAGAGCAGTTTGTAAAAAATTCAT
 TAGCATGAAGGCAAGCATATTTCTCTCATATGAATGAGCCTATCAGCAGGCTCTAGTTTCTAGG
 AATGCTAAAAATCAGAAGGCAAGGAGAGGAGATAGGCTTATATGATACATAGTGAGTACATTAAAGTA
 AAAATAAATGGACCTGCTTATCTTTTGGTGTGCTCTTTAACTGTCTCCGTTTTTTCTTTTAAAAAAT
 GCATTTTTTTTTCTGTGAGTTATAGTCTGCTTATTTAATTACCACTTTCGCAAGCTTACAAGAGA
 GCACAAAGTTGGCCTACATTTTTATTTTTTAAAGAGATACCTTTGAGATGCAATATGAGAACTTTCA
 TTTCAAAGCATCAAATTTGATGCATATCCAAGGACATGCCAAATGCTGATCTGTGCAGGCATGAAT
 CTGAGGCATTTGAGACATAGGGAAGGAATGGTTGTACTAATACAGACGTACAGATACCTTTCTGTAA
 GAGTATTTTCAAGAGGAGCACTGAACACTGGAGGAAAGAAATGACACTTCTGCTGCAACCAATCTCT
 AAGGAAACTCATTCAGACTGTGTGATTCGTGATGTACCTAAAGTCAAGAACCAATTTCTCTCA
 GAAGTAGGGACCGCTTTTCTCTCTGCTTCTGGCTTCCATAAGAAGAAATGGAGAAAAATATATAT
 ATATATATATATTGTGAAGATCAATTCATCTGCCAGAATGTGGGATGGAAGTTTGTGTACAT
 GTTATGCCCCAGGCGGAGAGTAAGTAACTGAATATTTTTTAAATTAAGCAGTTCTACTCAATCA
 CCAAGATGCTTCTGAAAATGCAATTTATACCAATTTCAAACCTATTTTTTAAAAAATAACAGTA
 ACATAGAGTGGTTTCTTCATTCATGTGAAAATATTAGCCAGCACCAGATGCATGAGCTAATTTATCT
 CTTTGAGTCTCTGCTTCTGTTTGTCTCAGTAACCTCATTTGTTTAAAGCTTCAAGAACTTCAAGC
 TGTGGTGTGTTAAAAAATGCATTTGATTTGATGTTGATGTTGATGTTTATGAATTTAATAAAAAC
 AGGCCATGAATGAAGGTGGTATTGCACAGCTAATAAAATATGATTTGTGGATATGA

0000504.41404

MMVMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQALPRANSPTGKEGYQAVLQ
EWEEQHRNYVSSLLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFL
HSQVDKAEVNAAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPRVKDKRDELVEAIES
ALETLNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSP
MKVKNEKLNMANLTINVIPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVK
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTR
LNTQPGKKVFYPVLSQYNPGIIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI
NIGGFDLDIKGWGGEDVHLRYRKLHNSLIVVRTPVRGLFHLWHEKRCMDELTPEQYKMCMS
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSKKT

FIGURE 277

GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTGCTGAACTCTGTCAACC
AGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT
ATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA
GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTTACTTTGCAATGTAACCCAGAGGGT
ATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCTGCTGTTGAGGTGC
AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAAT
CTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCATCTG
GATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTAT
CAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGAT
AAGTGTGAAAACATGATCACAAATTGAAAATGGCATCCCTCTGATCCCTGGACATGAAGGG
GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT
TGTTCTGCTTCTCAAGAAATTAAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATA
CCAAGAGCAGATCATATATTTTGTTCACCATCTTCTTTTGTAAATAAATTTTGAATGTGCT
TGAAAGTGAAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTACAGAC
TCAAAATATTCTAAAATATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTG
TAGTTATTGATTTAAGCATTTTTAGAAATAAGATCAGGCATATGTATATATTTTACACTTC
AAAGACCTAAGGAAAAATAAATTTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCAT
TGAAAATGGATCCTTTTTTGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAG
TGAGAAGTAATTATTGTAAATGGATGGATAAAATGGAATTACTCATATACAGGGTGGAATT
TTATCTGTTATCACACCAACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGAC
AATTCTATTTGTTGACCATTTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAG
TAATAATCATCTCTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 279

AAC TCAAAC TCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGGAGTGGCCTTGGCAGT
GTGTTGGAGCCCTCGGTCTGCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTC**ATGT**
ATGGCAAGAGCTCTACTCGTGCGGTGCTTCTTCTCCTTGGCATACAGCTCACAGCTCTTTGG
CCTATAGCAGCTGTGGAAATTTATACCTCCCGGTGCTGGAGGCTGTTAATGGGACAGATGC
TCGGTTAAAAATGCACTTTCTCCAGCTTTGCCCTGTGGGTGATGCTCTAACAGTGACCTGGA
ATTTTCGTCTCTAGACGGGGACCTGAGCAGTTTGTAATCTACTACCACATAGATCCCTTC
CAACCATAGAGTGGGCGGTTTAAGGACCGGGTGTCTTGGGATGGGAATCCTGAGCGGTACGA
TGCCTCCATCCTTCTCTGGAACCTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGA
AGAACCACCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA
CGCTTCTCTGAGATCCACTTCTCTGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCAT
AATAGTAATTTAGTAGTGGTCCCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC
ATAAAGTGGTGGAGATAAAATCAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCT
GTTTATTTAGAAGACACAGAC**TAA**CAATTTTAGATGGAAGCTGAGATGATTTCCAAGAACAA
GAACCCTAGTATTTCTTGAAGTTAATGGAAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGT
TTTCCAACCAAGTTCTGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC
AGTGCTCCTCCATATCACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTTCAGA
GTGTAAATTTTTCAAGTGCTCATTAGGTTTTATAACAAGAAGCTACATTTTTGCCCTTAA
GACACTACTTACAGTGTTATGACTTGTATACACATATATTGGTATCAAAGGGGATAAAAGCC
AATTTGTCTGTTACATTTCTTTACGTATTTCTTTTAGCAGCACTTCTGCTACTAAAGTTA
ATGTGTTTACTCTCTTCTCCACATTCTCAATTAAAGGTGAGCTAAGCCTCCTCGGTG
TTTCTGATTAACAGTAAATCCTAAATCAAAGTGTAAATGACATTTTTATTTTATGTCTC
TCCTTAAGTATGAGACACATCTGTTTTACTGAATTTCTTCAATATTCCAGGTGATAGATT
TTTGTGCG

FIGURE 280

[illegible]

FIGURE 281

GCATTTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACC**ATGA**AAGTTCTTAGCAGTCCTGGT
ACTCTTGGGAGTTTCCATCTTTCTGGTCTCTGCCCAGAATCCGACAACAGCTGCTCCAGCTG
ACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCCTGATGCTGAAACCACTGCTGCT
GCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG
TAAAGACATTCCAGTTTTACCCAAATGGGTTGGGGATCTCCCGAATGGTAGAGTGTGTCCC**T**
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACATATTCATGCTTCCTGTGATTTC
ATCCAACACTACTTACCTTGCCTACGATATCCCCTTTATCTCTAATCAGTTTATTTTCTTTCAA
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

MKFLAVLVLLGVSIFLVSAQNPTTAAPADTYPATGPADDEAPDAETTAATTATTAAPTTAT
 TAASTTARKDIPVLPKWVGDLPNGRVCP

FIGURE 283

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCAAGGAAGTGTTCCAACCTTGACCC
CTAGGGGTCTGGATTTGCTGGTTAACAAGATAACCTGAGGGCAGGACCCCATAGGGGAAATGC
TACCTCCTGCCCTTCCACCTGCCCTGGTGTTCACGGTGGCCTGGTCCCTCCTTGCCGAGAGA
GTGTCCTGGGTGAGGACGCGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC
ACTTGCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG
GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGCCAGTCCAGGGTGGGGGGCG
GCAAACCTCCATAAAGAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCATCTGCCCAGCTCCT
CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAGTAAACCACAGGCTGG
ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA
CCCCAAGAGCTTTCATTGTATCTATTGATTTTTACCACATTAGCAATTAACCTGAGAAAT
GGGCCGGGCACGGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT
CACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTACTAAAAA
TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCAGTTACTCGGGAGGCTGAG
GCAGGAAAATCGCTTGAACCCAGGAGGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT
TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

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FIGURE 284

MLPPALPPALVFTVAWSLLAERVSQWRDAEDAHRLQPFVTERTLGKVQRWSGVHTQTGGRAG
GGQFCCAWLDSKRVLASPGWGAANSIKNQRVWAPATESSAQLCCWPVGVARGGALCQ

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FIGURE 285

GTCATGCCAGTGCCTGCTCTGTGCCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA
GCGGCCCCCATGGGCGGCCCAGAACTGGCACAGCATGAGGAGCTGACCCTGCTCTCCATGG
GACCCTGCAGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGACGGCTGACAA
AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGGCAGGAGGTCAGC
CGGGGCCGGGATGCAGCCCAGGAACCTTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA
TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCAGGCACAGA
AGGTGCTACGGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT
GCCTACCGAGAATTTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC
CCTCACAGGCCACGTGCAGCGGCAGAGGCGGGAGATGGTGGCACAGCAGCATCGGCTGCGAC
AGATCCAGGAGAGACTCCACACAGCGGCGCTCCAGCCTGAATCTGCCTGGATGGAAGTGA
GACCAATCATGCTGCAAGGAACACTTCCACGCCCCGTGAGGCCCTGTGCAGGAGGAGCTG
CCTGTTCACTGGGATCAGCCAGGGCGCCGGGCCCCACTTCTGAGCACAGAGCAGAGACAGAC
GCAGGCGGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGGTGGAGGAAGGACATGTA
CCCTTTTCATGCCTACACACCCTCATTAAGCAGAGTCGTGGCATTTCAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAA

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FIGURE 286

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTLLEFHGTLQLGQALNGVYRTTEGRLTK
ARNSLGLYGRTIELLGQEVSRGRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAAQQHRLRQ
IQERLHTAALPA

FIGURE 287

GGCAACATAGCGCTCAGCAGGCTTGCCCCAGAGCCATGCGCAAGGAATGGAGTTGTAAATTTGCAT
CCTGGTGTATCACCCTTACTCCTGGACCAGACCACCAGCCACACATCCAGATTTAAAGGCCAGGA
AGCACAGCAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTTGAAAAGCTC
TGGACAGAAGTCAATGCCTTGAAGGAAATTCAGCCCTGCAGACAGTCTGTCTCCGAGGCAC
TAAAGTTCACAAGAAATGCTACCTTGCTTCAGAAAGTTTGAAGCATTTCATGAGGCCAATG
AAGACTGCATTTCCAAAGGAGGAATCCTGGTTATCCCCAGGAACCTCCGACGAAATCAACGCC
CTCCAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGA
CATGGTCACGGAAGGCAAGTTTGTGTACGTCAACGGAATCGCTATCTCCTTCCCTCAACTGGG
ACCGTGCACAGCCTAACGGTGGCAAGCGAGAAAACCTGTGTCTGTCTCCCAATCAGCTCAG
GGCAAGTGGAGTGATGAGGCCTGTGCGACGAGCAAGAGATACATATGCGAGTTCACCATCCC
TAAATTAGGTCTTTCTCCTCAATGTGTCTCCTCCAAGCAAGATTCATCATAACTTTATAGGTTTATGA
TCTCTAAGATCAAGTAAAAATCATAATTTTACTTATTAAAAAATTTGCAACACAAGATCAAT
GTCCATAGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTTGGCCT
TCTTGGGGTATAGGGGATCAGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCT
AAACAGACTAAAATCTTTCTCTCTAGTCTTTTCTCACTTGTACAAACCCAGCTTTGTTTTCAA
AAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT
TTCCTTGGAGTTTAGCGTATGTTTGACTAACAAAAATTCCTACATCAGAGACTCTAGGT
GCTATATAATCCAAAACCTTTTCAGCCTGTGTCTCATTCTGTCCCATGCTGGCAATAATACC
TTGTGAGCCCATTAACCCTTATTTTGAATTGCTCCATCTCCTGGTGGGACTTGTATCTTGTCT
GCCATATCAGAACACAACCCCTGAAGAGGTTCTGATTTGATTTTTTTTTTTTCTTTCATGCC
TACCCTTTTTTTTGGAGTTTCCAGCCGCAATTTGAAATGAAATGACAAGGTGTATATTGAT
CAATTTTTCATTCCCACCATTCGATTACAACCTCTAACTTAAATGGGTAAACCTTAAGGCATAT
CAAAGAAGCAGATTGCATGATAACGGAAATAGAAAAAAGAACCTACATTTATTTTGCTTT
AGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCTTTTTTACATTT
TCGTATATTTATTTTTTTTAGCCATCATTATATGTTTAAGTCTATTATGGGCAACCAATCTT
TGGAGCTGAAAACGAATTTAAGAATGCTATCTTGGAAAATTGCATACGCTGTGCAATT
TTTTATTCTGCCTAGTGCTATTCTGCTTGTTTAACTAGATTGTACAAAATAACTTCATTGCT
TAATATCAAATTACAAAGTTTAGACTTGGAGGGAAATGGGCTTTTTAGAAGCAAACAATTTT
AAATATATTTTGTCTTCAAATAAATAGTGTTTAAACATTGAATGTGTTTTGTGAACAATAT
CCCACCTTTGCAAACCTTAACTACACATGCTTGGAAATTAAGTTTtagctgttttcattgctca
ATAATAAAGCCTGAATTCGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 288

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHSKRRVRDKDGLKTQIEKLWT
EVNALKEIQALQTVCLRGTKVHKKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQ
DYGKRSLPGVNDFWLGINDMVTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFSSAQGK
WSDEACRSSKRYICEFTIPK

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MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHSKRRVRDKDGLKTQIEKLWT
EVNALKEIQALQTVCLRGTKVHKKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQ
DYGKRSLPGVNDFWLGINDMVTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFSSAQGK
WSDEACRSSKRYICEFTIPK

SCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGACAGTTCCCCGCGCGC
CCCCAGCCCCCGGCC**ATGA**AGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCTTGCA
GCTCCGCTGCTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCTGTGCTGCGCTG
GAGTCGGCGGCGGAGGCCGGGGCCGGGACCCTGGCCAACCCCCCTGGCACCCTCAACCCGCT
GAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGT
GTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG
GCCCTGACAGTGTTTGGC**TGA**GCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC
CACC CGCAGGGCTGAAAACCCCGCCGCGGGGAGGACCGTCCATCCCCTTCCCCGCGCCCT
CTCAATAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAA

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FIGURE 290

MKLAALLGLCVALSCSSAAAFVLGSAKPVAQPVAALESAAEAGAGTLANPLGTINPLKLLS
SLGIPVNHLIEGSQKCVaelGPQAVGAVKALKALLGALTVFG

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FIGURE 291

TGAAGGACTTTTCCAGGACCCAAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCAC
 CCTTGGCCTCCGAGCCGATCACATGAAGGTGGTGCCAAGTCTCCTGCTCTCCGTCTCCTG
 GCACAGGTGTGGCTGGTACC CGGCTTGGCCCCAGTCCCTCAGTTCGCCAGAGACCCAGCCCC
 TCAGAACCAGACCAGCAGGGTAGTGCAGGCTCCAGGGAGGAAGAGGAAGATGAGCAGGAGG
 CCAGCGAGGAGAAGGCCGGTGAGGAAGAGAAAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTT
 GCCAAGGAGACTTCAAACCTCGGATTACGCTGCTGCGAAAGATCTCCATGAGGCACGATGG
 CAACATGGTCTTCTCTCCATTGGCATGTCCTTGGCCATGACAGGCTTGATGCTGGGGGCCA
 CAGGGCCGACTGAAACCCAGATCAAGAGAGGGCTCCACTTGCAGGCCCTGAAGCCCAACAAG
 CCCGGGCTCTGCTTCCCTCTTTAAGGGACTCAGAGAGACCTCTCCCGCAACCTGGAAC
 TGGGCTCTCAGAGGGAGTTTGGCTTCATCCACAAGGATTTTGATGTCAAAGAGACTTCT
 TCAATTTATCCAAGAGGTATTTTGATACAGAGTGCGTGCCATGTAATTTTCGCAATGCCTCA
 CAGGCCAAAAGGCTCATGAATCATTACATTAACAAAGAGACTCGGGGAAAATTTCCAAACT
 GTTTGATGAGATTAATCCTGAAACCAAATTAATTCCTTGTGGATTACATCTTGTCAAAGGGA
 AATGGTTGACCCCATTTGACCTGTCTTCACCGAAGTCGACACTTTCCACCTGGACAAGTAC
 AAGACCATTAAAGGTGCCCATGATGTACGGTGCAGGCAAGTTTGGCTCCACCTTTGACAAGAA
 TTTTCGTTGTCATGTCCTCAAACCTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCTCTCA
 TGGAGAAAATGGGTGACCACCTCGCCCTTGAAGACTACCTGACCACAGACTTGGTGGAGACA
 TGGCTCAGAAACATGAAACCCAGAAACATGGAAGTTTCTTTCCGAAGTTCAAGCTAGATCA
 GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAAGAATCTTCTCACCTTTG
 CTGACCTTAGTGAACCTCTCAGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTTACGAAGA
 ACAGTGATTGAAGTTGATGAAAGGGGCACTGAGGCAGTGGCAGGAATCTTGTGAGAAATTAC
 TGCTTATTCATGCCTCCTGTATCAAAGTGGACCGGCCATTTTATTTCATGATCTATGAAG
 AAACCTCTGGAATGCTTCTGTTTCTGGGCGGGTGGTGAATCCGACTCTCCTATAATTCAGG
 ACATGCATAAGCACTTCGTGCTGTAGTAGATGCTGAATCTGAGGTATCAAACACACACAGGA
 TACCAGCAATGGATGGCAGGGGAGAGTGTTCTTTTGTCTTAACTAGTTTAGGGTGTCTC
 AAATAAATACAGTAGTCCCACCTTATCTGAGGGGGATACATTCAAAGACCCCGAGCAGATGC
 CTGAAACCGTGGACAGTGCTGAACCTTATATATATTTTTTCTTACACATACATACCTATGAT
 AAAGTTTAATTTATAAATTAGGCACAGTAAGAGATTAACAATAATAACAACATTAAGTAAAA
 TGAGTTACTTGAACGCAAGCACTGCAATACCAACAGTCAAACCTGATTATAGAGAAGGCTA
 CTAAGTGACTCATGGGCGAGGAGCATAGACAGTGTGGAGACATTGGGCAAGGGGAGAATTCA
 CATCCTGGGTGGGACAGAGCAGGACGATGCAAGATTCATCCCCTACTCAGAATGGCATGC
 TGCTTAAGACTTTTAGATTGTTTATTTCTGGAATTTTTCATTAAAGTTTTTGGACCATGGT
 TGACCATGGTTAACTGAGACTGCAGAAAGCAAAACCATGGATAAGGGAGGACTACTACAAA
 GCATTAAATTGATACATATTTTTTAAAAA

FIGURE 292

MKVVP S L L S V L L A Q V W L V P G L A P S P Q S P E T P A P Q N Q T S R V V Q A P R E E E E D E Q E A S E E K A G E
E E K A W L M A S R Q Q L A K E T S N F G F S L L R K I S M R H D G N M V F S P F G M S L A M T G L M L G A T G P T E T Q I
K R G L H L Q A L K P T K P G L L P S L F K G L R E T L S R N L E L G L S Q G S F A F I H K D F D V K E T F F N L S K R Y F
D T E C V P M N F R N A S Q A K R L M N H Y I N K E T R G K I P K L F D E I N P E T K L I L V D Y I L F K G K W L T P F D P
V F T E V D T F H L D K Y K T I K V P M M Y G A G K F A S T F D K N F R C H V L K L P Y Q G N A T M L V V L M E K M G D H L
A L E D Y L T T D L V E T W L R N M K T R N M E V F F P K F K L D Q K Y E M H E L L R Q M G I R R I F S P F A D L S E L S A
T G R N L Q V S R V L R T V I E V D E R G T E A V A G I L S E I T A Y S M P P V I K V D R P F H F M I Y E E T S G M L L F
L G R V V N P T L L

FIGURE 293

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCAGACATGAG
GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG
CACCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG
GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTCTGTTCCC
TGTCAGAAGCCGAAACTCTTGACCACCAGGAGAAGCCACGAGGTCAGGGCAGGGGCCCCA
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCCCTGGGCCGTGTCTGAGTCCC
GAGCCCGACCATGACAGCCTGTACCACCCCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCC
CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACA
TCTACACCCCCAGTAGGGCTCCAGGGGCCATCACTGCCCCGCCCTGTCCCAAGGCCCAGG
CTGTTGGGACTGGGACCCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCAGCAGGCAAA
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FIGURE 294

MRLLLLVTSLVVLLWEAGAVPAPKVPIKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVL
FFVQKPKLLTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEFDHDSLYHPPFEEDQGEE
RPRLWVMPNHQVLLGFEEDQDHIYHPQ

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FIGURE 295

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGAGTGAAGGAGCTCTCTG
 TACCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGC
 TGTTCCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA
 TGGACCTGTTCTTCGTCTCCATCTCTGCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC
 TAGTGCATTTGATGGCCTGTATTTCTCCGCACTGAGAATGGTGTTATCTACCAGACCTTCT
 GTGACATGACCTCTGGGGGTGGCGGCTGGACCTGGTGGCCAGCGTGCATGAGAATGACATG
 CGTGGGAAGTGCACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC
 AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCG
 ATGACTACAAGAACCCTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG
 CCAATAAGTCCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC
 TGGCTTCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTAAAT
 ATGGAGAAGGAAAGTGTTGGACTGACAACGGCCCGGTATCCCTGTGGTCTATGATTTGGC
 GACGCCCAGAAAACAGCATCTTATTACTCACCTATGGCCAGCGGGAATTCATGCGGGATT
 TGTTCA GTTCAGGGTATTTAATAACGAGAGAGCAGCCAACGCCTTGTTGTCTGGAATGAGG
 TCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAGGATACTTCCAGAGGCCAGT
 CCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATATGGAACCTCATGTTGGTTA
 CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTTGAGAGTTTTGTG
 GGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAACAACCTTACCCA
 GTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGAAAAAAA

FIGURE 296

MNQLSFLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN
GVIYQTFCDMTSGGGGWTIVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFG
SAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGI
YQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYYSPIYQREFTAGFVQFRVFNNERAAN
ALCAGMRVTGCNTEHHCIGGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSSSREITEAAVLL
FYR

FIGURE 297

GCGGAGCCGGCGCCGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCC
CACGAGGCTGCCGCATCCTGCCCTCGGAACAATGGGACTCGGCGCGCGAGGTGCTTGGGCCG
CGTGCTCCTGGGACGCTGCAGGTGCTAGCGTGCTGGGGGCCGCCCATGAAAGCGCAGCC
ATGGCGGCATCTGCAAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAAC
AGAGACTCTCCAACATGTGCCTTCTGACCATACAAATGAAACTTCCAACAGTACTGTGAAAC
CACCAACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG
GCATCTAATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC
TACACCCAAAACAACAAGTGTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG
TAACCCACAATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAACATATGCAT
TCTGAAGCAAAGAAAGGATCAAAATTTGATACTGGGAGCTTTGTGGTGGTATTGTATTAAAC
GCTGGGAGTTTTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTC
GGTATCGAACCATAGATGAACATGATGCCATCATTAAAGGAAATCCATGGACCAAGGATGGA
ATACAGATTGATGCTGCCCTATCAATTAATTTTGGTTTATTAATAGTTTAAAACAATATTCT
CTTTTGGAAATAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTA
AAGATTCTTCAAGGTAACAAGGTTTGGGTTTTGAAATAAACATCTGGATCTTATAGACCGT
TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAACAAGTCCTATCTTTTTTTTTTGCT
GGGTGGGGCATTGGTCACATATGACCAGTAATTGAAAGACGTCACTACTGAAAGACAGAA
TGCCATCTGGGCATACAATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTGT
AGCTCACATAAAGAACTTCAGTGCTTTTCAGAGCTGGATATATCTTAATTAATGCCACA
CAGAAATTATACAATCAAACCTAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTG
TGCTTTAACTGTAGTAGTTGGTCTAGAAACAAAATACTCC

FIGURE 299

CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGG
 TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCAGCG**ATG**CGGACCCTGTGGGGAGGC
 CTTCTTCGGCTTGGCTCCTTGTCTAGCCTGTCGTGCCTGGCGCTTCCGTGCTGCTGTGGC
 GCAGCTGTCTAGACGCCGCCAAGAATTCGAGGATGTCTAGATGTAATGTATCTGCCCTCCCT
 ATAAAGAAAATCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCCTT
 CATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGA
 ATGCAAATATGAAGAAAGAAGCTCTGTCTACAATCAAGGTTACCATTATAATTTATCTCTCCA
 TTTTGGGCCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG
 CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACACAGCCTTT
 TGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACTGCTGAACAAGGTAG
 AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGG
 CATGTTGTCTCTAGC**TAA**TTGGGAATTGAATTCAGGTGACTAGAAAGAAACAGGCAGACAA
 CTGGAAGAAGTACTGAGGTTTTGCTGGGTTTCATTTTAATACCTTGTGATTTACCAACT
 GTTGCTGGAAGATTCAAAAGTGAAGCAAAAAGTCTGCTTATTTTTTTTCTTGTAAACGTA
 ATAATAGAGACATTTTTAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCTTATTG
 TGACTTTTACTAATAAAAAATAAATCTGCCTGTAATATCTTGAAGTCTTTACCTGGAACA
 AGCACTCTCTTTTCCACCACATAGTTTAACTTGACTTTCAAGATAATTTTCAAGGTTTTTG
 TTGTTGTTGTTTTTTGTTTGTGTTTTGTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGT
 AACAAGTTTTTTCAAGTCACCTTACTAAACAACTTTTGTAATAGACCTTACCTTCTATTT
 TCGAGTTTCATTTATATTTTGCAGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTG
 ACTTTTGCAGTACTGTATTATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGAT
 CTAAATGCCTGGTGGCTTTTACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATG
 CAATGCATCCTAGAACAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTG
 GTGTGTGTTGTTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACT
 TGCAATAAAGAAATTTTATTTTAAACCCAGCCTCCCTGGATTGATAATATATACACATTTG
 TCAGCATTTCCGGTCTGGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAAGT
 AGGGCTGGGGTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTT
 TCTTCTATGTCCTCTTTGGAATGTAACAATAAAAAATAATTTTGAACATCAA

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FIGURE 300

MATLWGGLRLGSLLSCLALS VLLLAQLSDAAKNFEDVRCKCICPPYKENS
GHIYNKNIS
QKDCDCLHVVEFMPVRGPDVEAYCLRCECKYEERS SVTIKVTII IYLSILG
LLLLYMVYLT
LVEPILKRRLF GHAQLIQSDDDIGDHQPFANAHDV LARSRSRANVLNKVEYA
QQRWKLQVQEQ
RKSVFDRHVVL S

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FIGURE 301

GCACCTGCGACCACCGTGAGCAGTCCATGGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT
CTGGGCTTGTCCTGGCTCTGTCGCTGCTGCTGCCAAGGCCTTCCTGTCCCGCGGGAAGCGG
CAGGAGCCGCCGCCGACACCTGAAGGAAAATTGGGCCGATTTCCACCTATGATGCATCATCA
CCAGGCACCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGG
CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGAAGAGGTCTG
ATGGGGCAGATTATTCCAATCTACGGTTTTTGGGATTTTTTTATATATACTGTACATTCTATT
TAAGGTAAGTAGAATCATCCTAATCATATTACATCAATTGAAAATCTAATATGGCGATAAAAA
TCATTGCTTACATTAAAACCTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTA
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTCAAGTTTCACATAAGAATG
TTTACTCAATGTTTAAGTGTTTTTGCCCCAAAATTCACAACCTAACAGGCAGAACTAGGACTT
GAACATGGATCTTTGGTTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

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FIGURE 302

MAYSTVQRVALASGLVLALSLLLPKAFLSRGKRQEPPPTPEGKLGFRFPPMHHHQAPSDGQT
PGARFQRSHLAEAFKAKGSGGGAGGGSGRGLMGQIIPYGFIFLYILYILFKVSRILI
ILHQ

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FIGURE 303

CGGCTCGAGTGCAGCTGTGGGGAGGATTTCAGTGCAATTGCCTCCCTGGGTGCTCTTCATCTT
GGATTTGAAAGTTGAGAGCAGCATGTTTTGCCCACTGAAACTCATCCTGCTGCCAGTGTTAC
TGGATTATTCTTGGGCCCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTCCATGTG
GGTGATTCAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATATTCAAGAT
AGACTGGACTCTGTCAACAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCA
ATCTCAGTGTGCCTATTGGGCGCTTCCAGAACC CGGTACACTTGATGGGGGACATCTTATGC
AATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA
AATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAG
AGGAGCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTGAGATGGGATGTGTTTTCCAG
AGCACAGAAGTGAAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGA
GGAGATTGTATTTTGTTACTACCAAACTCAGGATGTCTGTGGAGTACTCCAGAGCTGGG
GCCACTTCCAGAATCGTGTGAACCTGGTGGGGACATTTTCCGCAATGACGGTTCCATCATG
CTTCAAGGAGTGAGGGAGTCAGATGGAGGAAACTACACCTGCAGTATCCACCTAGGGAACCT
GGTGTTCAAGAAAACCATTTGTGCTGCATGTCAGCCCGGAAGAGCCTCGAACACTGGTGACCC
CGGCAGCCCTGAGGCCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTC
TGTGCCACAATCCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAAATAA
GAGTTCAGTGAATTTCTACAGTCTTGGTGAAGAACCGAAGAAGACTAATCCAGAGATAAAAG
AAAAACCTGCCATTTTGAAGATGTGAAGGGGAGAAACACATTTACTCCCAATAATTGTA
CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCA
CCCACTTTGGCCTTCTCTGAGGTGAGATCGGAACAACTCACTTGAAAAAAAGTCAGGTGGG
GAATGCCAAAAACAGCAAGCCTTTTGAAGAAGAATGGAGAGTCCCTTCATCTCAGCAGCGG
TGGAGACTCTCTCCTGTGTGTGCTCTGGGCCACTCTACCAGTGATTTGAGACTCCGCTCTC
CCAGCTGTCTCCTGTCTCATTGTTTTGGTCAATACACTGAAGATGGAGAATTGGAGCCTGG
CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGC
CTCTGGAGTGGGACACTGGGCCTGGGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCCGTT
GGATCAGACCCTCCTGTGGGCAGGTTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATA
AAAACCAACCCAAATCAA

FRANCIS CHAMBERLAIN, JR., President, American Society of Mechanical Engineers, New York, N. Y.

FIGURE 305

CTATGAAGAAGCTTCCTGGAAAAACAATAAGCAAAGGAAAAACAAATGTGTCCCATCTCACATG
GTTCTACCCCTACTAAAGACAGGAAGATCATAACTGACAGATACTGAAATTGTAAGAGTTGG
AAACTACATTTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCCATGCA
GGATGAAGATGGATACATCACCTTAAATATTAAACTCGGAAACCAGCTCTCGTCTCCGTTG
GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGG
ATGGTTGTCGGGCTGGTGGCTCTGGGGATTGGTCTGTCATGCAGCGCAATTACCTACAAGA
TGAGAATGAAAATCGCACAGGAACCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG
TAAACAATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCCTGTGACACAAAC
TGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACCTAACATGGGAAGAGAG
TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG
AGTACATCAAAGCCAGGACTCATTTAATTTCGTGGGTGGGATTATCTCGCCAGAAGTCGAAT
GAGGCTCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGAAGA
TGGAAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCTACCTTCTGTG
AGAACAACATTATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT
TAATGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAAGATATGT
ATGAATGCATCAGTAGCTGAAAAAAAAAAAAA

FIGURE 306

MQDEDGYITLNIKTRKPALVSVGPASSSWWRVMAILLILCVGMVVGLVALGIWSVMQRNYL
QDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSYGFRRHNLWE
ESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEFL
EDGKGNMNCAYFHNGKMHPTECENKHYLMCERKAGMTKVDQLP

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FIGURE 307

CCCACGCGTCCGCGCAGTCCGCGAGTTCTGCCTCCGCTGCCAGTCTCGCCCGGATCCCGG
CCCCGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGGGAGCCGGACCGC
CGCCGGAGGAGCTCGGACGCGATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTGC GGAGAA
GCCCCGGCAAACGCGAGGCTAAGGAGACCAAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAG
CGGAGGAGAAGGAGGAGGAGGCGAACCCAGAGAGGGGCAGCAAAAGAAGCGGTGGTGGTGGG
CGTCGTGGCC**CATG**CGGCGGCTATCGCCAGCTCGCTCATCCGTGAGAAGAGGCAAGCCCGCG
AGCGCGAGAAATCCAACGCCTGCAAGTGTGTGAGCAGCCCCAGCAAGGCAAGACCAGCTGC
GACAAAACAAGTTAAATGTCTTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG
AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGTACC
ACTTGCAGCTGCAGGCGGATGGAACCATGTGATGGCACCAAAGATGAGGACAGCACTTACACT
CTGTTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACCTTTTACACCTGAGTGCA
AATTCAAAGAATCAGTGTGTTGAAAATTATTATGTGACATATTCATCAATGATATACCGTCAG
CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGT
ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC
AAGAGCAGAAGTGTCTCTGGCGTGCTGAACGGAGGCAAATCCATGAGCCACAATGAATCAAC
GTAGCCAGTGAGGGCAAAAGAAGGGCTCTGTAAAGAACCTTACCTCCAGGTGCTGTTGAAT
TCTTCTAGCAGTCCTTCAACCAAAAGTTCAAATTTGTGAGTGACATTTACCAACAAACAGG
CAGAGTTCACCTATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

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FIGURE 308

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498

><subunit 1 of 1, 245 aa, 1 stop

><MW: 27564, pI: 10.18, NX(S/T): 1

MAAAIASSLIHQKQAREREKSNACKCVSSPSKGKTSCDKNKLNVFSRVKLFSGSKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLIQVGLRVVAIQGVQTKLYLA
MNSEGILYLTSELTPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLENKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKRSVSVGLNGGKSMHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

FIGURE 309

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGG
ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGG
CAACCTGGATATTCTGAGACATATTTTGGGGGATTTCAGTGAAAAAGTGGGGGATCCCCCT
CCATTTAGAGTGTAGCAAAGGAAAAACACCAAGGTTGGGTTTCCTTCTCTGACATTGGCAGTG
CCCCAGTAGGGGTGGGATGAGCGAATATTCCTAAAGCTAAAGTCCCACACCCTGTAGATTAC
AAGAGTGGATTTGGCAGGAGTGTGCCCCAAAATACAGTGGAAGGTGCCTGAAGATATTTAA
ACCACGTCTTGGAATTTAGTGGGTCTTGCTTTGGGATAGGTGAAGTGAGGACAGACACTG
GAGAGGAGGAAAGGGGACGTTTTCAATAGGAGGCAAACTCGAGGGTGGGATCCACTGAGG
AGTACATAGGCTGTGGATCTGGTGGAGCCAGCACTGGGCCACGGGTGGTAAGTGGCTGCT
GTGGAGGGGGGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGGTCTGTGGGTGGGGCAG
CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCAG
CGCGCTCCGGGCGCCTGCCGTTTGGGGGTGTCTCCTCCGGGGCGCTATGGCGGGCGCTGGC
CAGTAGCCTGATCCGGCAGAAAGCGGGAGGTCCGCGAGCCCGGGGGCAGCCGGCCGGTGTCCG
CGCAGCGGCGCGTGTGTCCCCGGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCCTG
CTGTCCAAGGTGCGACTGTGCGGGGGGCGGCCCGCGCGCCGACCGCGGCCCGAGCCTCA
GCTCAAAGGCATCGTACCAAAGTGTCTGCGGCCAGGGTTTCTACCTCCAGGCGAATCCCG
ACGGAAGCATCCAGGGCACCCAGAGGATACCAGCTCCTTCACCCACTTCAACCTGATCCCT
GTGGGCTCCGTGTGGTACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGC
TGAGGGACTGCTCTACAGTTCGCGCATTTACAGCTGAGTGTGCTTTAAGGAGTGTGTCT
TTGAGAATTACTACGTCTGTACGCCTCTGCTCTTACCGCCAGCGTCGTCTCTGGCCGGGGC
TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTATGAAGGAAACCGAGTTAAGAAGACAA
GGCAGCTGCCCACTTTCTGCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC
ACAGTGTCCCGAGGCCTCCCCTTCCAGTCCCCCTGCCCTCGAATGTAGTCCCTGGACTG
GAGGTTCCCTGCACTCCAGTGAGCCAGCCACCACCACAACCTGT

FIGURE 310

MAALASSLIRQKREVREPGGSRPVSAQRRVCPRGTKSLCQKQLLILLSKVRLCGGRPARPDR
GPEPQLKGIVTKLFCRQGFYLOANPDGSIQGTPEDTSSFTHEFNLI PVGLRVVTIQSAKLGHY
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNR
VKKTAAAHLPLKLEVAMYQEPSLHSVPEASPSPPAP

Tyrosine kinase phosphorylation site:

amino acids 199-207

N-myristoylation sites:

amino acids 54-60, 89-95, 131-137

HBGF/FGF family signature:

amino acids 131-155

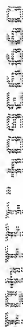


FIGURE 311

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGGGAGCAGCACTG
GGACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACC GCGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA
GTAAAGAAAACCAAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGGAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGCCTCTGCAATAATGAATGGAGGCAAACCAGTCAACAAGAGTAAGACAACA**TAG**

FIGURE 312

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWDPSASRRSSPSKNRGLCNGNLVDIFSKVRIFGLKKRRLR
RQDPQLKGIVTRLYCRQGYLQMHPDGDLDGTDKDDSTNSTLFNLIPVGLRVVAIQGVKTGLY
IAMNGEGYLYPSELFTECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVFKPGVTPSKSTSASAIMNGGKPVNKSKT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

FIGURE 313

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAAT
 GAAGGATGACGAGCGCAGCTTTCTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGA
 ACGAAGCTTTTTCTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGAGCATTCAAGAATG
 AAATAAACAGAGTTAGACCCGCGGGGTTGGTGTGTTCTGACATAAATAAATAATCTTAAAGCAGCTGTTCCC
 CTCCCCACCCCCAAAAAAGGATGATTGGAATGAAGAACCAGGATTACAAAGAAAAAGTATGTTCAATTT
 TTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTTGAATGAAAAGTTTGGGGCTTTTTTAGTAAAGTAA
 AGAACTGGTGTGGTGGTGTTTTCCTTTCTTTTTGAATTTCCACAGAGGAGAGGAATTAATAATACATCTGC
 AAAGAAATTTAGAGAGAAGAAAGTTGACCGCGGAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCA
 CAGTTGGATTTGTGCTTATGTTGACTAAAATGACGGATAATTGCAGTTGGATTTTTCTTCATCAACCTCCTTT
 TTTTAAATTTTATTCCCTTTGGTATCAAGATCATGCGTTTCTCTGTTCTTAACCACCTGGATTTCATCT
 GGATGTTGCTGTGATCAGTCTGAAATACAACCTGTTGAATTCAGAGGACCAACACCAGATAAATATGAATG
 TTGAACAGATGACCTTACATCCACAGCAGATAATGATAGTCTTAGGTTTAAACAGGGCCCTATTGACCCCT
 GCTTGTGGTGTCTGCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGGGGCTCAGACCTGCCCTTCTGTGT
 GCTCCTGCAGCAACAGTTGAGCAAGTGATTGTGTTGCGAAAACTGCGTGAGGTTCCGGATGGCATCTCC
 ACCAACACACGGCTGCTGAACCTCCATGAGAACCAATCCAGATCATCAAGTGAACAGCTTCAAGCACTTGAG
 CCACTTGGAAATCCTACAGTTGAGTAGCAACCATATCAGAACCATTGAATTTGGGGCTTCAATGGTCTGGCGA
 ACCTCAACACTCTGGAACCTCTTGACAATCGCTTACTACCATCCGGAATGGAGCTTTGTATACTTGTCTAA
 CTGAAGGAGCTCTGGTTGCGAAACAACCCATTGAAAGCATCCCTTCTTATGCTTTTAAAGAAATTCCTTCTTT
 GCGCCGACTAGACTTAGGGGAATTGAAAGACTTTCATACATCTCAGAGGTGCCTTTGAAGGCTGTGCCAAT
 TGAGGTATTTGAACCTTGCCATGTGAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAACTAGATGAG
 CTGGATCTTTCTGGAATCATTTATCTGCCATCAGGCTGGCTCTTCCAGGGTTGATGCACCTTCAAAACT
 GTGGATGATACAGTCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGTGAGATCA
 ACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTTGACATCATCTAGAGCGGATACAT
 TTACATCACAACTTGGAACTGTAAGTGTGACATATCTGCGTCAAGTGGTGAATAAAGACATGGCCCCCTC
 GAACACAGCTTGTGTGCGCGGTGTAACACTCCTCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGA
 ATTACTTCACATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCT
 GAGCTGAAATGTGCGGCCCTCCACATCCCTGACATCTGTATCTTGATTACTCCAATGGAACAGTCATGACACA
 TGGGGCGTACAAAGTGGCGATAGCTGTGCTCAGTGATGGTACGTTAAATTTCAAAATGTAAGTGTGCAAGATA
 CAGGCGATGTACATGATGTTGGTGAAGTAATCCGTTGGGAATACTACTGCTTCAGCCACCTGAAATGTTACTGCA
 GCAACCACTACTCCTTTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGACG
 GACCACAGATAAAGTGGGTGCCACTCCAGTGGTGGTGGGAGACCAATGTGACCACTCTCTCACAC
 CACAGAGCACAAAGTGCAGACGAAAACTTCAACATCCAGTGACTGATATAAACAGTGGGATCCCGGAATT
 GATGAGGTCAAGAGACTACCAAAATCATCATTTGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCT
 GGTCAATTTCTACAAGATGAGGAAGCAGCACCATCGGCAAAACCATCAGGCCCAACAAGGACTGTTGAAATTA
 TTAATGTGGATGATGAGATTACGGGAGACACACCATGGAAGCCACCTGCCCATGCTGCTATCGAGCATGAG
 CACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCACACAACACAGTTAAACACAATAAATCAATACA
 CAGTTCACTGATGAACCGTTATTGATCCGAATGAACCTTAAAGACAATGTACAAGAGACTCAAACTTAAACA
 TTTACAGAGTTACAAAAACAAACAATCAAAAAAAGACAGTTTATTAAAAATGACACAAATGACTGGGTAA
 ATCTACTGTTTCAAAAAGTGTCTTTACAAAAAACAAAAAGAAAGAAATTTATTATTAAAAATTTCTATTG
 TGATCTAAAGCAGACAAAA

FIGURE 314

MLNKM TLHPQQIMIGPRFNRLFDPLLVL LALQLLVVAGLVRAQTCPSVCSNQSFKVIC
 VRKNLREVDPGISTNTRLLNLHENQIQIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
 NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
 YISEGAFEGLSNLRYINLAMCNLREIPNLTPLIKLDLDELDSGNHLSAIRPGSFQGLMHLQKL
 WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPNWNCNDIL
 WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
 LKCRASLTLSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVDGMYTCMVSNVSGN
 TTASATLNVTAATTTFSYFSTVTVETMEPSQDEARTDNNVGPTPVVDWETTNTVTTSLTPQ
 STRSTEKTFITPVTIDNSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHRQN
 HHAPTRTVEIINVDDEITGDTPMESHLMPAIEHEHLNHNYSYKSPFNHTTTVNTINSIHSS
 VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
 434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
 391-397, 422-428, 433-439, 531-537

FIGURE 315

GCGCGGGGAGCCCATCTGCCCCAGGGGCACGGGGCGGGGGCCGGCTCCCGCCCGGCACAT
 GGCTGCAGCCACCTCGCGCGCACCCGAGGCGCGCGCCAGCTCGCCCGAGGTCCGTCCGA
 GGGCGCCGCGCCCGCGGAGCCACAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATC
 GGGATGTCCTCCTCCTTCTCCTCTTGTAGTTTCTTACTATGTTGGAACTTGGGGACTCA
 CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACCTTGGCCTGCCACCATCAACTGGGGC
 TTCCAGAAAAGACACTCTGGATATTGAATGGCTGCTCACCATAATGAAGGGAACCAAAAA
 GTGGTGATCACTTACTCCAGTCGTCATGCTACAATAACTTGACTGAGGAACAGAAGGGCCG
 AGTGGCCTTTGCTTCCAATTTCTCGGAGGATGCTCCTTGCAGATTGAACCTCTGAAGC
 CCAGTGATGAGGGCCGTACACCTGTAAGGTTAAGAATTGAGGGCGCTACGTGTGGAGCCAT
 GTCATCTTAAAGTCTTAGTGAGACCATCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC
 AGAAGGAAGTGACCTGACCTTGGCAGTGTGAGTCATCCTCTGGCACAGAGCCCCATTGTGTATT
 ACTGGCAGCGAATCCGAGAGAAAAGGGAGAGGATGAACGTCTGCCTCCCAAACTCTAGATT
 GACTACAACCACCCTGGACGAGTTCTGCTGAGAATCTTACCATGTCTACTCTGGACTGTA
 CCAGTGCACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTCCGAGTAACGTGTACAGT
 ATGTACAAAGCATCGGCATGGTTGACAGGAGCAGTGCAGGCATAGTGGCTGGAGCCCTGTGTG
 ATTTTCTCCTTGGTGTGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGA
 GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCGCTCTGTGAAACCCAGCT
 CCTCTTCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCTCCTCCACTCGCTCCACAGCAAAT
 AGTGCCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCAC
 CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAGAAAGTCCACCATG
 CTAATCTGACCAAGCAGAAACCAACCCAGCATGATCCCCAGCCAGAGCAGAGCCTTCCAA
 ACGGTCTGAATTACAATTGACCTTGAACCTTCTCCTAGGAGTCAGGGTCTTTGGACTC
 TTCTCGTCATTGGAGCTCAAGTCACCCAGCCACCAACAGATGAGAGGTCATCTAAGTAGCA
 GTGAGCATTGCACGGAACAGATTCAGATGAGCATTTTCTTATACAATACCAACAAAGCAAA
 AGGATGTAAGCTGATTATCTGTAAAAGGCATCTTATTGTGCCCTTAGACCAGAGTAAGGG
 AAAGCAGGAGTCCAAATCTATTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTG
 AGGTGAATATACCTAAACTTTTAAATGTGGGATATTTTGTATGATTTCTGCAAACTTATTGGATT
 TTCAAGAGGAAATGGGATGCTGTTGTGAAATTTCTATGCATTTCTGCAAACTTATTGGATT
 ATTAGTTATTTCAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTAC
 TGAGCTAACCACTTCTAAGAACTCCAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC
 TTCATTTGTCTAAGGTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGATGGAGA
 AGAGTGAATGAGTTTCTCCCACTCTATACTAATCTCACTATTTGTATTGAGCCCCAAATAAC
 TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCCATCTTCTATGATT
 ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTCCCTCAAAT
 CAGATGCCCTTAGGACTTTCTGCTAGATATTTCTGGAAGGAGAAAATACAACATGTCTATT
 TATCAACGTCCTTAGAAAAGAACTTTCTAGAGAAAAAGGATCTAGGAATGCTGAAAGATTA
 CCCAACATACCATTATAGTCTCTTCTTCTGAGAAAATGTGAAACAGAAATTGCAAGACTGG
 GTGGACTAGAAAGGGAGATTAGATCAGTTTCTCTTAATATGTCAAGGAAGGTAGCCGGCA
 TGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAGGTGCACTGAGCCGAGATTATGCC
 ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

FIGURE 316

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLVSYYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELTEGSDTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVVRVTQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANS
ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

FIGURE 318

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361

><subunit 1 of 1, 352 aa, 1 stop

><MW: 38938, pI: 7.86, NX(S/T): 3

MALLLCFVLLCGVDFARSLSITTPPEEMIEKAKGETAYLPCKFTLSPEDQGPLDIEWLISPA
 DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTLQLSDIGTYQCKVKK
 APGVANKKIHVLVLKPSGARCYPDVGSEEIGSDFKIKCEPKESLPLQYEWQKLSDSQKMPT
 SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSQCLLRNLNVPPSNKAGLIAGAIIGTLL
 ALALIGLIIFCCRKKRREEKYEKEVHHDIREDVPPPKSRTSTARSYIGSNHSSLGSMSPSNM
 EGYSKTQYNQVPSSEDFERTPQSPSTLPPAKFKYPYKTDGITVV

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
 245-251, 296-302

Myelin P0 protein.

amino acids 96-125

FIGURE 319

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGA
ATGGTGAAGGTGCCTGTCTAACTTTTCTGTAAAAAGAACAGCTGCCTCCAGGCAGCCAGCC
CTCAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTCGC
CAATTTAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTG
AGAG**ATGA**AATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCTTCTGCCCTC
CTTTGCTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCTGGGTTTTACCCTG
CTTCTCTGGAGCCAGGTATCAGGGGGCCAGGGCCAAGAATCCACTTTGGGCCCTGCCAAGT
GAAGGGGGTTGTTCCCCAGAAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG
CTCAGGATAACATCACGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGAT
GCTGAGAGCTGTTACCTTGTCCACACCTGCTGGAGTTCTACTTGAAACTGTTTTCAAAAA
CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACT
TTGTTCTCATCGTGTCAACTGCAACCCAGTCAAGAAATGAGATGTTTTCCATCAGAGAC
AGTGCACACAGGCGGTTTTCTGCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGC
TCTGACCAAAGCCCTTGGGGAAGTGGACATTCTCTGACCTGGATGCAGAAATTCTACAAGC
T**CTGA**ATGTCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTTTTGTTCCCTGTGTCATTTCA
AACAGTCTCCCTTCCCTATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATTCT
TTGGCCCAGGATTATTGTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG
GTGCCTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTTGATTTATTACAACCTCTATTT
AATTAATGTCAGTATTTCAACTGAAGTTCTATTTATTTGTGAGACTGTAAGTTACATGAAGG
CAGCAGAATATTGTGCCCCATGCTTCTTTACCCCTCACAACTCTTGCCACAGTGTGGGGCAG
TGGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATT
GTTAAAAACAGAGAGGGATGCTTGGATGTAAACTGAACTTCAGAGCATGAAAATCACACT
GTCTTCTGATATCTGCAGGGACAGAGCATTGGGGTGGGGTAAGGTGCATCTGTTTGAAAAG
TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAAGCAGATCCTCAATAAACATTTTCATT
TCCCACCCACACTCGCCAGCTCACCCCATCATCCCTTTCCCTTGGTGCCCTCCTTTTTTTTT
TATCCTAGTCATTCTTCCCTAATCTTCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGAC
ATTGCACCTGGATGTACTATCCAATCTGTGATGACATTCCCTGCTAATAAAAGACAACATAA
CTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

320/330

FIGURE 320

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRLQSLWTLARPFPCPELLATASQMOMVVLPCLGFTLLLWSQVSGAQGQEFHFGPCQVK
GVVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYLYKTVFKNH
HNRTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAAL
TKALGEVDILLTWMQKFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

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FIGURE 321

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGCCATGAAGTTACAGTGTGTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGCTTGATTTC
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCAAATGTCACTATCCTGTCCACATTGGGAGACTCTGCAGATCATTAAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAAGGATCA
TCAGGAGCCAAACCCCAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCTCTACA
TGCAGAAAACCTCTGCGGCAATGTGAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACATATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCTTGGGAGAGCTCGACGTCTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT
GTGGGAGACAGCCACCTTGAAGGGAAGGAGATGGGGAAGGCCCTTGACAGTGAAAGTCC
CACTGGCTGGCCTCAGGCTGTCTTATTCGCTTGAAAATAGGCAAAAAGTCTACTGTGGTAT
TTGTAATAAACTCTATCTGCTGAAAGGGCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT
CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATCCATATTTTACCTATGA

FIGURE 322

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282

><subunit 1 of 1, 177 aa, 1 stop

><MW: 20452, pI: 8.00, NX(S/T): 2

MKLQCVSLWLLGTLILCSVDNHGLRRCLISTDMHHIBESFQEIKRAIQAKDTFPNVITILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHNDYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

FIGURE 323

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG
AACCGGGCTACAATTAATACATAACCTTATGTATCATACATACGATTTAGGTGACACTAT
AGAATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAACATGCACCTC
GGTTCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGGCCCGCCT
CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCA
ATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCC
AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGAC
CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA
TGAGCAGAAGATACCTCTGCATGGATTTAGAGGCAACATTTTGGATCACACTATTTTCGAC
CCGGAGAACTGCAGGTTCACACACCAGACGCTGAAAAACGGGTACGACGTCTACCACTCTCC
TCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACC
CACCCCGTACTCCAGTTCCCTGTCCCGGAGGAACGAGATCCCCCTAATTCACCTCAACACC
CCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCTGAACGT
GCTGAAGCCCCGGGCCCCGGATGACCCCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCG
CCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTGAGTGAAC
ACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCTTCGCCAAGTTCATCTAGGGTGC
CTGG

FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGHVD
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLENGY
DVYHSPQYHFLVSLGRAKRAFLPGMNPPYPYSQFLSRNEIPLIHFNTPIPRRHTRS AEDDSE
RDPLNLVKPRARMT PAPASCSQELPSAEDNSPMASDPLGVVRGGRVNT HAGGTGPEGCRPFA
KFI

Important features of the protein:**Signal peptide:**

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

FIGURE 325

GGAAAAGGATACCCGCGAGAGACGCCAGCAGTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATC**
GGCTGTCTCTGGGGTCTGGCTCTGCCCTTTTCTTCTCTGTCTGGGAGGTTGGGGTCTCTGG
GAGCTCTGCAGGCCCCAGCACCCGCAGAGCAGACACTGCGATGACAACGGACGACACAGAAG
TGCCCGCTATGACTCTAGCACCGGGGCCAGCCGCTCTGGAAACTCAAACGCTGAGCGCTGAG
ACCTCTTCTAGGGCTCAACCCAGCCGGCCCCATTCCAGAAGCAGAGACCAGGGGAGCCAA
GAGAATTTCCCCTGCAAGAGAGACCAGGAGTTTCAAAAAACATCTCCCAACTTCATGGTGC
TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
ACAGTTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCCTTTGCACCGA
TGACAGCTCTGAAGAGGCAAAAGACACTACAATGGACATATTGACATTGGCTCACACCTCCA
CAGAAGCTAAGGGCCTGTCTCAGAGAGCAGTGCTCTTCCGACGGCCCCCATCCAGTCATC
ACCCCGTACAGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATACCCC
GTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATACCCCGTCAT
GGTCCCCGGGATCTGATGTCACTCTCCTCGCTGAAGCCCTGGTGACTGTCACAAACATCGAG
GTTATTAATTGCAGCATCACAGAAATAGAAACAACACTTCCAGCATCCCTGGGGCCTCAGA
CATAGATCTCATCCCCACGGAAGGGGTGAAGGCCCTCGTCCACCTCCGATCCACCAGCTCTGC
CTGACTCCAATGAAGCAAAACCACACATCACTGAGGTCACAGCCTCTGCCGAGACCCTGTCC
ACAGCCGGCACACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCCACTAA
CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCCTCAGTGGAGCTCTGGTCA
CAGTTAGCAGGAATCCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC
AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTCAGCAGTGGGCAAAAACAATT
CTTTGCTGGGAGCTCTGCTTCTCTACAGCCCCTCGGAAGCCGCCCTCAAGAACTTCACCC
CTTCAGAGACACCGACCATGGACATCGCAACCAAGGGGGCCCTTCCCCACAGCAGGGACCCCT
CTTCTTCTGTCTCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA
GATCACAACTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCCACGACTGCCCGGAC
GAGGCCGACCACAGACGT**TGA**GTGCAGGTGAAAATGGAGGTTTCTCTCTCTGCGGCTGAGTG
TGGCTTCCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGTGATGCAGCAGCTCCAC
CGGGAATCCACGCCACGCGCCTCACTTCCAGGTCTCCTTACTGCGTGTGAGGAGAGGCTA
ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGCTGCTGCCCTAGCCTG
GGCCCCACCGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
AAGGGCAGCATGTCCAAGCCCTAACCCAGATGTGGCAACAGGACCCTCGCTCATATCCAC
CGGAGTGTATGTATGGGGAGGGGCTTCACTGTTCAGAGGTGTCTTGGACTCACCTTGG
CACATGTTCTGTGTTTCAGTAAAGAGAGACCTGATACCCATCTGTGTGCTTCCATCTGCA
TTAAATTCACCTCAGTGTGGCCAAAAAAA

FIGURE 326

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALETQTL
 ETSSRASTPAGPIPEAETRGAKRISPARETRSFTKTSNFMVLIATSVETSAASGSPEGAGM
 TTVQTIITGSDPEEAIFDTLCTDDSSSEAKTLTMDILTTLAHTSTEAKGLSSESSASSDGP
 HPVITPSRASESSASSDGPHPVITPSRASESSASSDGPHPVITPSWSPGSDVTLLEALVT
 VTNIEVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVT
 ASAETLSTAGTTESAAPHATVGTPLPTNSATEREVTAPGATTLGALVTVSRNPLEETSAL
 SVETPSYVKVSGAAPVSI EAGSAVGKTTSFAGSSASSYSPSEAAALKNFPTSETPTMDI
 ATKGPFPSTRDPLPSVPPTTTNSSRGTNSTLAKITTSKTTMKPQQPRRLPGRGRPQT

N-glycosylation sites:

amino acids 252-256, 445-449, 451-455

cAMP-and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-90

Casein kinase II phosphorylation sites.

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,
 246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,
 404-408, 414-418, 431-435

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-
 320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

FIGURE 327

GCGGAGCATCCGCTGCGGTCTCGCCGAGACCCCGCGCGGATTGCGCGGTCTTCCC GCGG
 GCGCGACAGAGCTGTCTCGACCTGGATGGCAGCAGGGGCGCCGGGGTCTCTCGACGCCA
 GAGAGAAATCTCATCTCTGTGCAGCCTTCTTAAAGCAAATTAAGACCAGAGGGAGGATTAT
 CCTTGACCTTTGAAGACCAAACTAAACTGAAATTTAAA**ATG**CTCTTCGGGGGAGAAGGGAG
 CTTGACTTACACTTTGGTAATAATTTGCTTCCCTGACACTAAGGCTGTCTGCTAGTCAGAATT
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCTTACATCCAGTCATCTCTTTCTAAGGGGAATC
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATTCCTTGCTGTTCAAC
 AAAAAACATATCAGGGGACAAAGCATGTAACCTTGATGATCTTCGACACTCGAAAAACAGCTA
 GACAACCCAACTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAGCA
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
 CCAAGAGTTACCCCAAGGAAGATTCTCTCTTACATGGCCAATTTTCACAAGCAGTCACCTCCC
 TAGCCCATCATCACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCT
 CAGAAGTTTGGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAATTTTCTCTGATCAAGAAA
 TAGCTCATCTGCTGCCTGAAAATGTGAGTGCGCTCCAGCTACGGTGGCAGTTGCTTCTCCA
 CATACCACCTCGGCTACTCCAAAGCCCGCCACCTTCTACCCACCAATGCTTCAGTGACACC
 TTCTGGGACTTCCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAAACCACTGTCACTTCTC
 AGCCTCCCACGACCCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG
 GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA
 AACCATACCGTTTACAGAAATCTCCAACCTTAACCTTGAACACAGGGAATGTGTATAACCTA
 CTGCACTTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTGGGAAGGT
 AGGGAGGCCAGTCCAGGCAGTTCTCTCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCC
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGCTCTGTTCTGTTGATAGGCC
 TCGTCTCCTGGGTAGAATCCTTTCGGAATCACTCCGAGGAACGTTACTCAAGACTGGAT
 TATTTGATCAATGGGATCTATGTGGACATC**TAAG**GATGGAACCTCGGTGTCTCTTAATTCATT
 TAGTAACCAGAAGCCCAAATGCAATGAGTTTCTGCTGACTTGTCTAGTCTTAGCAGGAGGTTG
 TATTTTGAAGACAGGAAAATGCCCTTCTGCTTCTTTTTTTTTTTGGAGACAGAGTCTT
 GCTCTGTGCCCAGGCTGGAGTGACGATAGCACGATCTCGGCTCTCACCGCAACCTCCGCTCTC
 CTGGGTTCAGCGATTCTCCTGCCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
 CCACACCTGGGTGATTTTTGTATTTTTAGTAGAGACGGGGTTTACCATGTTGGTCAGGCTG
 GTCTCAAACCTCCTGACCTAGTGATCCACCCTCCTCGGCTCCCAAAGTGCTGGGATTACAGG
 CATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTTGGTTTTTGAGAAGGAATGAAGTG
 GGAACCAAAATTAGGTAATTTTGGGTAATCTGTCTCTAAATATTAGCTAAAAACAAAGCTCT
 ATGTAAAGTAATAAGTATAATTGCCATATAAATTTCAAATTCACCTGGCTTTTATGCAAA
 GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATTCCTGGTTCCAGATAAAATCAAC
 TGTTTATATCAATTTCTAATGGATTGCTTTTTCTTTTATATGGATTCTTTTAAACTTATT
 CCAGATGTAGTTCTTCCAATTAAATATTGAATAATCTTTTGTTACTCAA

0003604-11167

FIGURE 328

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410

><subunit 1 of 1, 431 aa, 1 stop

><MW: 46810, pI: 6.45, NX(S/T): 6

MFFGGEGSLTYTLVIICFLTLRLSASQNCCLKSLEDVVIDIQSSLSKGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLHGGFSQAVTFLAHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSPPTTLISTVFTRAAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPFEKWLIGSLLFGVLFLVLVIGLVLLGRILSESLRRKRYSRDYLINGIYVDI

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

330/330

FIGURE 330

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLVLVLLWGCLLLPGYEALLEGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS
GTIYAEEEGQETMKGRVSIRDSTRQELSLIVTLWNLTLDAGEYWCVEKRGPDSELLISLFV
FPGPCCPPSPSPPTFQPLATTRLQPKAKAQQQTQPPGLTSPGLYPAATTAKQKGTGAEAPPLPG
TSQYGHERTSQYTGTSPHPATSPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIIPMVRI
LAPVLVLLSLLSAAGLIAFCSHLLLRKEAQQATETQRNEKFWLSRLTAEKEAPSQAPEGD
VISMPPLHTSEEEELGFSKFVSA

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128